

**FIGURE 1**

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA  
CCTGGTGCACCACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG  
GTTTTCCACCAGCTTTTACCAAGGCCTCCCCTGTTGTGAAGAATTCCATCACGAAGAATCA  
ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA  
GAACTGGCCAAGAAGCTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAATATTTAAAATT  
GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA  
CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT  
ATGTCAAGGATAGAATTCAATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT  
TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACCTCATGATGAGAGGCTCTTG  
GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC  
CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT  
GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC  
AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAAAGTTTCTGA  
ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCCTCATTTGGGATCTATG  
TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT  
AGTTCTTTTTCAGCATGTTCTTCTGTATGATAACCAGAAAGTAATCAAGCGTGCAGAAAGTAT  
CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACCTCGATGCTGAGTATCTACATGGAT  
ACATTAAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAA**ATG**  
**A**AGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAAATGGGGCAGATATGC  
ATTAAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA  
TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT  
AATCCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAAATGTT  
TTGGTGAATGTGAAAATAAAGTTTGTGTCATGAGAATGTAAAGTCTTTTTTCTACTTTAAAA  
TTTAGTAGGTTCACTGAGTAACTAAAATTTAGCAAACCTGTGTTTGCATATTTTTTTGGAGT  
GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG  
GAGTCACCTGCAGTCTTTTGTTTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA  
GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGAAACAAGTGGTCATTGTTACATTCATTT  
GCTGAACTTAACAAAAGTGTTCATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG  
CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC  
ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA  
ATAACTTTAAAAGTATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTTCCAG  
AATACAAACAGTATACTCATG

**FIGURE 2**

MLAARLVCLRTLPSRVFHPAFTKASPVVKN SITKNQWLLTPSREYATKTRIGIRRGRTGQEL  
KEAALEPSMEKIFKIDQMGRWVAVAGGA VGLGALCY YGLGLSNEIGAIEKAVIWPQYVKDRI  
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP  
GPKHLAWLLHSGVMGAVVAPLTI LGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL  
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLF SMFLLYDTQKVIKRAEVSPMYGV  
QKYDPINSMLSIYMDTLNI FMRVATMLATGGNRKK

**FIGURE 3**

GAAGGCTGCCTCGCTGGTCCGAATTCCGGTGGCGCCACGTCCGCCCGTCTCCGCCTTCTGCAT  
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCCGGCCGCGTCTGTAGGG  
 GGTCCGGCACGGGGAGTCCGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTCTGAAG**ATGT**CGG  
 ACATCGGAGACTGGTTCAGGAGCATCCCGGCGATCACGCGCTATTGGTTCGCCGCCACCGTC  
 GCCGTGCCCTTGGTTCGGCAAACCTCGGCCTCATCAGCCCGGCCTACCTCTTCTCTGGCCCGA  
 AGCCTTCTTTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG  
 GTCCAGGAACCTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGCGA  
 CTTGAAACAGGAGCTTTTGTGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG  
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA  
 TGTCAGTACTTTATGTCTGGGCCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGG  
 ACACGATTTAAGGCCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG  
 CTCGGTAATCAATGAGCTTATTGAAATCTGGTTGGACATCTTTATTTTCTTAATGTTCA  
 GATACCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG  
 CTGCCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC  
 TGCTGATCAGAATGGCGGAGGCGGGAGACACAACCTGGGGCCAGGGCTTTGCACTTGGAGACC  
 AG**TGA**AGGGGGCGGCCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCTCTCCAGTGCTGGGTG  
 CACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTT  
 AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCACAAAGTTTCACGAT  
 TCTCATTTCAAGTCCCTTACTGCTGTGAAGAACAATACCAACTGTGCAAAATGCAAACTGAC  
 TACATTTTTTGGTGTCTTCTCTTCTCCCTTTCCGTCTGAATAATGGGTTTTAGCGGGTCCT  
 AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAAACCTTCCCAAAAGGACCTTATCTCTT  
 TCTTGACACATGCCTCTCTCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG  
 CCCATAAAATGTCTGCCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGTC  
 ACAACAATCATATTACGTTATTTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG  
 AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATTGCTTCGACTGACATCCGTTGTT  
 AACCGTTTGGCACTCTTCAGATATTTTTTATAAAAAAAGTACCACTGAGTTCATGAGGGCCA  
 CAGATTGGTTATTAATGAGATACGAGGGTGGTGTGTTGTTTCTGAGCTAAGTGA  
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC  
 TTTGCGTTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT  
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCTGGGCATTG  
 ATTCCCATTTCAATCTCATTCTGGATATGTGTTTCATTGAGTAAAGGAGGAGAGACCCTCATA  
 CGCTATTTAAATGTCACTTTTTTGCCCTATCCCCGTTTTTTGGTTCATGTTTCAATTAATTGT  
 GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAACACATCTA  
 AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGAGGGTGTGTTA  
 TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTT  
 TCGTAGGTGGGCTTTTCCATACAGAGCTTGGCTCATAACCAAATAAAGTTTTTTGAAGGCCA  
 TGGCTTTTACACAGTTATTTTATTTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT  
 ATTGAGTGGCTGTACACTTTGAGGCAACTAAAAAGGCTTCAAACGTTTGTATCAGTTTCTT  
 TTCAGGAAACATTGTGCTCTAACAGTATGACTATTCTTTCCCCCACTCTTAAACAGTGTGAT  
 GTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTTGTGTG  
 TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTCA  
 TGTTTTGTTGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAAATTTTAGAGGCCATTACT  
 CCAATTATGTTGCACGTACACTCATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATA  
 TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCCTCTTACCAGTCAGCTGCCTGCGAG  
 CAGTCATTTTTTCTTAAAGGTTTACAAGTATTTAGAACTTTTCAGTTCAGGGCAAAATGTTC  
 ATGAAGTTATTCCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGATT  
 ATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTTGACTTGACAAGGCAAAACA  
 TGACAGTGGATTCTCTTTACAAATGGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCC  
 TTTTGTAAACTAATCCTTTTTATTGGTAAAAATTGTAAATTAAATGTGCAACTTG

**FIGURE 4**

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLG LISPAYLFLWPEAFLYRFQIWRPITATFYF  
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP  
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIIGGSVINELIGNLVGHLYFFL  
MFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRLL  
GDQ

**Transmembrane domain:**

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

**FIGURE 5**

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG  
GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT  
CCTTGTGGCCCAAAGGCCTAACCAGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTTGCC  
CCTTTGGGGCGGGATGGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG  
CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT  
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT  
GGCCTGTGTTCCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC  
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT  
AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC  
CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA  
AAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTACCT  
GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT  
GAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA  
AACAGTTATCAGAGGCTAAACAGAAGAGCCCACAGTGCATTCCAGTGAAGCTGCAATAATG  
AATAATTCCCAAGGGGATGGTGAACATTTTGCACACCCACCCTCAGAAGTTAAAATGCATTT  
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCCTCCCTCC  
CACAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC  
TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA  
TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG  
GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG  
CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAGTA  
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC  
CTTACACTG

**FIGURE 6**

MAAEEDEVEWVESIAGFLRGPDSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP  
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP  
VLAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGVLPDCLTDGSDVVSDLEHEEMKILREVL  
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS  
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS  
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRRLLAEKLKEEVINK

**N-glycosylation sites.**

amino acids 224-228, 246-250, 285-289

**N-myristoylation site.**

amino acids 273-279

**Amidation site.**

amino acids 252-256

**Cytosolic fatty-acid binding proteins.**

amino acids 78-108

### FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT  
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA  
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG  
GCCATTTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC  
AGAAAAACATTGAAATGCAGCTGCAAGCCATTCTGAATAATTCAAGAGAGAAATGGTGTATTA  
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT  
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

**FIGURE 8**

CCGTGGTTTTTTGTCTTGC AATAGGCGCTTAGAGGAGAGGGGCTTTTTCGCCTATACCTACTG  
TAGCTTCTCCACGTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG  
TCTCAGCTCTAGGATGTGCGTTCCTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAAC  
AGTGGA**ATG**GAAAAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC  
ATTCTTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT  
CTGCCAATGAAGAAAAACAAGTATGATTATCTTCCACTACTGTGAATGTGTGCTCAGAACTG  
GTGAAGCTAGTTTTCTGTGTGCTTGTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG  
AAATTTGAAATATGCTTCCTGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATTTCCTGCCT  
TTCTTTATTTCTTGATAACTTGATTGTCTTCTATGTCTGTCTATCTTCAACCAGCCATG  
GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAGGATAGTGCTGAA  
GAGGCGTCTAAACTGGATCCAGTGGGCTTCCTCCTGACTTTATTTTTTGTCTATTGTGGCCT  
TGACTGCCGGGACTAAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC  
TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCCAGAAAAGACAATTG  
TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTC  
ACATCCGTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTTATTTCTTCAATGGCT  
AATATCTATAATGAAAAGATACTGAAGGAGGGGAACCAGCTCACTGAAAGCATCTTCATACA  
GAACAGCAAACCTCTATTTCTTTGGCATTCTGTTTAATGGGCTGACTCTGGGCCTTCAGAGGA  
GTAACCGTGATCAGATTAGAAGTGTGGATTTTTTTTATGGCCACAGTGCATTTTCAGTAGCC  
CTTATTTTTTGTAACATGCATTCCAGGGCCTTTTCAGTGGCTTTTCATTCTGAAGTTCCTGGATAA  
CATGTTCCATGTCTTGATGGCCAGGTTACCACTGTCAATTATCACAACAGTGTCTGTCTCTGG  
TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGGAAGCCCCATCAGTCCTTCTCTCTATA  
TTTATTTTATAATGCCAGCAAGCCTCAAGTTCGGAATACGCACCTAGGCAAGAAAGGATCCG  
AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA  
CCAAACCCAAAGAGTGATGAGTCAGATGAAGATACTTTCT**TAA**CTGGTACCCACATAGTTTGCA  
GCTCTCTTGAACCTTATTTTACATTTTTCAGTGTGTTGTAATATTTATCTTTTCACTTTGATA  
AACCAGAAATGTTTCTAAATCCTAATATTCTTTGCATATATCTAGCTACTCCCTAAATGGTT  
CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTCTAAAGAACTGATACAGGAGTAACA  
ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT  
TTTCCTTGGCCTTCAAGCTTCCAAAAAACTTGTAATAATCATGTTAGCTATAGCTTGTATAT  
ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT  
CTTCCCTTTTTTAACATTATAAAAAGCTAGGTTGTCTCTTGAATTTTGAGGCCCTAGAGATAGT  
CATTTTGAAGTAAAGAGCAACGGGACCCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC  
CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAAATATTTTGCTGAAGAAGCAGT  
TTCTCAGACACAACATCTCAGAATTTTAATTTTTTAGAAATTCATGGGAAATTGGATTTTTGT  
AATAATCTTTTGATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTACCACTTGTATTTTA  
AGTCATTTAAACAAGCCACGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT  
GTCATTACTCCTGAATTATTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACT  
AATTCAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC  
CAGATTGTGAGTGAAGCTGATGCCTAGGAACTTTTAAAGGGATCCTTTCAAAGGATCACTT  
AGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAAGACC  
AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAAGTGCATGGTATTTTTTCATG  
GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA  
AAATTAGCAAACAAAAGTGAAGTGTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG  
CTTTAACTGGCAGGCCTGTATGTTTACAGACTACCATACTGTAAATATGAGCTTTATGGTGT  
CATTCTCAGAAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA  
AGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAATTG  
GTGGAAATTTGTAATTAAAATAATTATTAAACCT



**FIGURE 9**

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK  
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV  
IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF  
SPSNSCLLFRSECPRKDNTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI  
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI  
FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI  
YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESDETF

**Transmembrane domains:**

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,  
298-318, 328-368

**N-glycosylation sites.**

amino acids 128-132, 204-208, 218-222, 374-378

**Glycosaminoglycan attachment site.**

amino acids 402-406

**N-myristoylation sites.**

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

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**FIGURE 10**

CGTGCCCTGCGCAATGGGTGTCTGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG  
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC  
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG  
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAAACAGTGGAATGGAA  
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCCTGCTAGG  
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG  
AAAACAAGTATGATTATCTTCCAACACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT  
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA  
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCCTGCCTTTCTTTATTTCC  
TGGATAACTTGATTGTCTTCTATGTCCTGTCTTCTTCAACCAGCCATGGCTGTTATCTTC  
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAGGATAGTGCTGAAGAGGCGTCTAAA  
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA  
CTAAAACTTTA

**FIGURE 11**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC  
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCTGCGGGGCAGAGGAGCAT  
 CCCGTCTACCAGGTCCCAAGCGGCGTGGCCCCGCGGGTCATGGCCAAAGGAGAAGGCGCCGAG  
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCCCCGGCCCA  
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTTGCAACAAGCTTTGCTATG  
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC  
 CTATTGGATGTTGGCTCAGGTGGGCCCTTTCTCTGCCTCCATCATCCTGTTTGTGGGCCGAGC  
 CTGGGATGCCATCACAGACCCCCCTGGTGGGCCTCTGCATCAGCAAATCCCCCTGGACCTGCC  
 TGGGTCGCCTTATGCCCTGGATCATCTTCTCCACGCCCCCTGGCCGTCATTGCCTACTTCCTC  
 ATCTGGTTCGTGCCCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCCT  
 CTTTGAAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA  
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC  
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCTTGTTTCCAGG  
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACACATGGCACCACCTTCACAC  
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTG  
 TGCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTG  
 AGCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATAACATCAAACCTT  
 ATTACTGGCTTCCTCTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTT  
 TTGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAATCTACTCCTGGCCATCATGCTCT  
 CGGCCACTTTAACCATTCCCATCTGGCAGTGCTTCTTGACCCGGTTTGGCAAGAAGACAGCT  
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA  
 CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC  
 TACCCTGGTCCATGCTGCCTGATGTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT  
 GGAACCGAGCCCATCTTCTTCTCCTTCTATGTCTTCTTCACCAAGTTTGCCTCTGGAGTGTC  
 ACTGGGCATTTCTACCCTCAGTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC  
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG  
 CTGGGCCTGCTGCTCTTCAAATGTACCCCATTGATGAGGAGAGGCGGCGGCAGAATAAGAA  
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG  
 AGCTGGCTAGCATCCTCTAGGGCCCCGCCACGTTGCCCCGAAGCCACCATGCAGAAGGCCACAG  
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA  
 CTGAAGACTCAAGGAGGTGGCCCAGGACACTTGCTGTGCTCACTGTGGGGCCGGCTGCTCTG  
 TGGCCTCCTGCCTCCCCTCTGCCTGCCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA  
 TGCCAAGGACTGATCGGGCCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC  
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTGTATGTATATGTCTGTGAGCTA  
 TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

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**FIGURE 12**

MWLRWALS LPPSSCLWAE PGMP SQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG  
SCPTSHTARPIGT CFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL  
GTAIQGQIVGQADTPCFQDFNSSTVASQSANH THGTTSHRETQKAYLLAAGVIVCIYIICAV  
ILILGVREQREP YEAQQSEPIAYFRGLRLVM SHGPYIKLITGFLFTSLAFMLVEGNFVLFCT  
YTLGFRNEFQNL LLAIMLSATLTIP IWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI  
ITYAVAVAAGISVAA AFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG  
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL  
QALRDEASSSGCSETDSTELASIL

634660

**FIGURE 13**

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT  
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA  
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA  
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT  
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC  
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG  
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC  
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT  
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG  
GAACCGAGCCCCAT

**FIGURE 14**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT  
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATG  
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT  
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT  
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG  
CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA  
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGGAACTGAGTTGTTTAGG  
ACTTTCTATTGTGGCAAACCTTCAGAAAACAACCCTTTTGTGCTGCACATGTAAGTGGAGCTG  
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG  
CAGCCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG  
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTGGGACTG  
ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT  
ACTGCAGCAGAATGGTCTATGTCAATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA  
TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCTCTATGACACTG  
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTTGATGAAAGGAT  
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA  
TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA  
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA  
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

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**FIGURE 15**

MWWFQQGLSFLPSALVIWTSAAFI<sup>1</sup>FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI  
AAVLCIAT<sup>2</sup>IYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG  
AVLTFGMGSLYMFVQTILSYQM<sup>3</sup>QPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG  
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDFQKISLRVEANLHGLTLYD  
TAPCPINNERTRLLSRDI

10577 634660

**FIGURE 16**

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT  
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA  
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTTGAAGCAGT  
TACCAAGAATCTTCAACCCTTTCCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA  
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA  
GTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT  
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT  
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC



**FIGURE 17**

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG  
CCGGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC  
CTTCGCCTTGTACTTGCTGTGACGCGACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGG  
AGGCTGGAGGCAGGTGCTGTGGTTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG  
GTCCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCCCTGCTCTTCTGCGGCGCCTA  
CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCCT  
TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC  
TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT  
GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT  
TGAGACTTTTCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCAATTCTGAACATT  
CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT  
GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG  
TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCCTATTAAAAAATTT  
AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA  
CACATTGATCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA  
TGTGGTCCTCTAAAGCCCCCTCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG  
CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT  
TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT  
GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATT  
ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT  
ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGC  
AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT  
CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

**FIGURE 18**

MRPLLGLLLVFAGCTFALYLLSTRLPRGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYR  
KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLGALFGPWLGLLLCCVLTSVGATCCYLLSS  
IFGKQLVVSYPDPKVALLRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPIVQFF  
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ  
LNETSTANHIHSRKDT

### Important features:

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31.

Sugar transport proteins.

amino acids 162-172

**FIGURE 19**

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTTT  
CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA  
TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA  
TTTATGACAACTTTCAGAGACTGTTGATTGTTGGTGAGACAGACCGGCCATCAGTGTGGCATG  
TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC  
CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT  
TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT  
GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA  
GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC  
CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTCTGCC  
AACTGCACTGGCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA  
ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCCTGTTGGAGGAAGAGATTC  
AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG  
TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA  
CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTCACTCACCTGCCATTTCCAAAAGATG  
CCTCTTTAAACAAGTGCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG  
ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA  
GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCTG  
ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT  
GGAACCGCTTTCTCAGAACTGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA  
AAACCAGGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAAACTGCAAAAA

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPPQYPLLVVY  
KVLATLGLILLTAYFVIQPFSPPLAEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL  
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMILLEDAPRKFERLHPLVIKT  
GKPLLEEEIQHFCLCQYPEATEGFSEGGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELPV  
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHQCQSVAMP  
IEPGDIGYVDTTTHWKVYVIARGVQPLVICDGTAFSEL

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCGC  
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAGTTGTGATC  
AAGGGACACGTGGTTTTCCGAAC TGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT  
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAAACTTTTCAGAGACTGTTG  
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC  
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCCCCGCAGTATCCTCTCCTTATAGT  
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC  
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

**FIGURE 22**

CCCACGCGTCCGCCCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG  
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG  
 CCACTGGTGCGCACGCTGCTAGACCGTGCTATGAGCCGCTGGGGCTGCAGTGGGGACTGCC  
 CTCCCTGCCACCCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA  
 CACCCGAATGGCGCCACTTCATCGACAAACAGGTACAGCCAACC**ATGT**CCCAGTTTCAAATG  
 GACACGTATGCTAAGAGCCACGACCTTATGTGAGTTTCTGGAATGCCTGCTATGACATGCT  
 TATGAGCAGTGGGCAGCGGCGCCAGTGGGAGCGCGCCAGAGTCGTGCGGGCTTCCAGGAGC  
 TGGTGCTGGAACCTGCGCAGAGGCGGGCGCCTGGAGGGGCTACGCTACACGGCAGTGCTG  
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGCT  
 CGCCAGCCCATGTGGGGCTGGGGCGCTGAGGGACACTCCCATCCCCCGCTGGAACTGTCCA  
 GCGCCGAGACATATTCACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCCTAC  
 CTGGAAGCGACGCGTCTCCGAGACAATCTGGGTGAGGTTCCTTACACCCACCGAGGAGGC  
 CTCACTGCCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCACCCGAGTTGCTGCAGG  
 AGGACCAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCAGCAGAAGTG  
 GATGAGCAGCGTGAGAAGCTGGTGCTGTGCGCCGAGTGCCAGCTGGTGACGGTAGTGCCGT  
 GGTCCAGGGCTGCTGGAGGTCAACACAGAATGTATACTTCTACGATGGCAGCACTGAGC  
 GCGTGGAACCCGAGGAGGGCATCGGCTATGATTTCGGCGCCCACTGGCCAGCTGCGTGAG  
 GTCCACCTGCGGCGTTTCAACCTGCGCCGTTCAGCACTTGAGCTCTTCTTTATCGATCAGGC  
 CAACTACTTCTCAACTTCCCATGCAAGGTGGGCACGACCCAGTCTCATCTCCTAGCCAGA  
 CTCCGAGACCCAGCCTGGCCCCATCCACCCCATACCCAGGTACGGAACCAGGTGTACTCG  
 TGGCTCCTGCGCCTACGGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCCAGGAGAT  
 GCTGCGTGCTCAGGCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTTCGAGTACT  
 TGATGCAACTCAACACCATTTGCGGGGCGGACCTACAATGACCTGTCTCAGTACCCTGTGTTT  
 CCCTGGGTCTGTCAGGACTACGTGTCCCCAACCCTGGACCTCAGCAACCCAGCCGTCTTCCG  
 GGACCTGTCTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAGAAGT  
 ATGAAAGCTTTGAGGACCCAGCAGGGACCATTGACAAGTTCCACTATGGCACCCACTACTCC  
 AATGCAGCAGGCGTGATGCACTACCTCATCCGCTGGAGCCCTTCACTCCCTGCACGTCCA  
 AATGCAAAAGTGGCCGCTTTGACTGCTCCGACCGGAGTTCCACTCGGTGGCGGCAGCCTGGC  
 AGGCACGCCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTCTTCTACTTTCT  
 GACTTCTTGAGAAACAGAACGGTGGTGGCTGTCTCCAGCTGACCAACGAGAAGGT  
 AGGCGATGTGGTGCTACCCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCAGCC  
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCACTTTGGC  
 TACAAGCAGCGGGGGCCAGCCGCGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA  
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA  
 TCAGCAACTTTGGGCAGACTCCCTGTGAGCTGCTGAAGGAGCCACATCCAACCTCGGCTCTCA  
 GCTGAGGAAGCAGCCCATCGCCTTGACAGCCTGGACACTAACTCACCTAGCATCTCCAGCA  
 CCTGGACGAACTCAAGGCATTCTTCGAGAGGTTGACTGTGAGTGCCAGTGGGCTGCTGGGCA  
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAGACCCC  
 ACCATGGGCAGCCACAAGACGCAGCGACTGCTGAGTGGCCCGTGGGTGCCAGGCAGTGGTGT  
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAGCTGCTATTAGCGGTGGCCACTGGG  
 ATGGCAGCCTGCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC  
 CTTGATGTAGTAACCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG  
 GGACACCACGTGCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTGAGTAGGCCTGGCAC  
 CAAAGCCTGTGCAGGTCCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT  
 GAACTTGACATGGCTGTGTCTGGATCTGAGGATGGAAGCTGTGATCATAACACTGTACGCCG  
 CGGACAGTTTGTAGCGGCACTACGGCCTCTGGGTGCCACATTCCCTGGACCTATTTTCACC  
 TGGCATTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGAACAGCTCCTGGGGCC  
 CAGGTCACTACTCCTTGACCTGTATTGAGTCAATGGGAAGTTGCGGGCTTCACTGCCCT  
 GGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTTGTGTTGCTGGGCACCGCCAGT  
 GCGCCCTGCACATCCTCCAACATAACACACTGCTCCCGGGCGCGCCTCCCTTGCCCATGAAG  
 GTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCTCAGCCACGTGCTGGTGGGCTGGAGGA  
 TGGCAAGCTCATCGTGGTGGTGGCGGGGAGCCCTCTGAGGTGCGCAGCAGTTCGCGC  
 GGAAGCTGTGGCGGTCCTCGCGGCGCATCTCCAGGTGTCTCGGGAGAGACGGAATACAAC  
 CCTACTGAGGCGCGCT**TGA**ACCTGGCCAGTCCGGCTGCTCGGGCCCCGCCCCCGGCAGGCCTG  
 GCCGGGAGGGCCCCGCCAGAGTGGCGGGGAACACCCCGGGGTGGGCAGCCAGGGGGTGA  
 GCGGGGGCCACCTGCCCAGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG  
 GGCGGAAGTCCCGCCCCCTCGCCGGCTGAGGGGCGGCCCTGAGGGCCAGCACTGGCGTCT

**FIGURE 23**

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL  
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVNP  
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALETP  
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP  
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV  
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL  
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDL SKPIGVNPKHAQLVREKYESFEDPAGTIDKFH  
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADV KELIP  
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQQHRQALESEYVSAHLHEW  
 IDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP  
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF  
 SFSKDPTMGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVTALPRGKLL  
 SQLSCHLDVVTCLALDTCGIY LISGSRDTTCMVWRL LHQGGLSVGLAPKPVQVLYGHGA AVS  
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA  
 WERPGAQVTYSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA  
 PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS  
 GETEYNPTEAR

**N-glycosylation site.**

amino acids 677-681

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 985-989

**Tyrosine kinase phosphorylation site.**

amino acids 56-65, 367-376, 543-551

**N-myristoylation site.**

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,  
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,  
 873-879, 912-918, 954-960

**FIGURE 24**

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC  
CACGGCCCACCTTGTGAACTCCTCGTGCCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT  
CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCCTGGGGCTCTTC  
TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTT  
CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC  
GCACACTCCGTTACCACACTGGGTCAATTGGCATTGAGGCCCTCATCCTGACCCCTGTGCAG  
ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGC  
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC  
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA  
AATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGTCGTCCTGGACAAAGTCACAGA  
CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCCTGTCCTTCTTTT  
TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCCACCTCAACTATTAC  
TGGCTGCCCATCATGACCTCCATCCTGGGGGCCTATGTCATCGCCAGCGGCTTCTTCAGCGT  
TTTCGGCATGTGTGTGGACACGCTCTTCCTCTGCTTCCTGGAAGACCTGGAGCGGAACAACG  
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC  
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGAGCTCCGGCCCTGATCCAGGACTGC  
ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT  
AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG  
AGGCGGGCGGATCACCTGAGTCAGGAGTTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC  
GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTAC  
TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA  
TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA  
AAAGATTTTATTAAAGATATTTTGTTAATC



**FIGURE 25**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLG  
LFWTLNWVLALGQCVLAGAFASYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ  
IARVILEYIDHKLGRVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK  
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYY  
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKN  
EAPPDNKKRKK

**FIGURE 26**

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGT  
GGCT**ATG**TTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC  
TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT  
CAGTGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAACTGC  
ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG  
ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG  
CCAGTCAATGTTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA  
TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT  
CAGGAAATGACAGTGTGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA  
GTGGAGCAAACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT  
CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG  
CTTGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC  
CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCCTGCAGCG  
CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA  
CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC  
AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA  
GCGGCTCCAGGAGTTCCTTGACAGATGGGTCTTCCCCTGAAGCAGGTGAAGCAGAAGTTCC  
AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAATAAA  
TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAGCACAAAGTT  
TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT  
CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG  
TACCATGGCCTGGAACCTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC  
CTTTGCACCAACCTCGTCATCTCCCAGGGGCCTTTCTGTACTGCTCTCTCATGGAGGGCAC  
TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA  
AGTCCTTTGTGTGTTGACAAAGAACCGGCGCTGCAAACCTGCTGCCCCTGGTGATGGCTGCC  
CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC  
GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAAGAAGCAGCGGAAAGCACCAGCTCCCGGA  
TGCTGCACAACCATTTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT  
CTGGACGCACTTATTTCCCTCCTGTCC**TAG**GAATTTGATTCTTCCAGAATGACCTTCTTATT  
TATGTAACCTGGCTTTCATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT  
TTTTATTAAATAAAATGCTTATTTTAGGAAA

**FIGURE 27**

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF  
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD  
LEVPAIEDIFRDEEEDEEHSGNDSGSEPSEKRTRLEEEIVEQTMRRRQRREWEARRRDILF  
DYEQYEHGTSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRH  
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR  
LQEF LADMGLPLKQVKQKFQAMD ISLKENLREMI EESANKFGMKDMRVQTF SIHFGFKHKFL  
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNL DKLYHGLELAKKQLRATQQT IASCL  
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP  
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNF DLSVIELKAEDRSKFL  
DALISLLS

**FIGURE 28**

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCGCA  
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT  
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT  
GGTTCAGTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAACAGTTTC  
ATTATTTTATTCTCATAAAGTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT  
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA  
CGATACCC

**FIGURE 29**

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAAC  
 CACGAAGGGACGATACCAGAAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG  
 GCTGACTTTGGCTATAGAAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGGAAAGCTAA  
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAACAATT  
 GAGTAAAGTACGCTCCGGTCACCA**ATGG**TGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC  
 CTGCTCTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC  
 CAGCGGTGCCAACGGTGTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAG  
 CCTCTTCTCCGGCCGCCCCACGCCCTGCCCTGAGATCAGACCCTACATTAATATCACCATC  
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGG  
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG  
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC  
 GGCGAGGACTTCCAGACGCTGCTCTTCAAGAGGTCTTTGTGAACCTTGATGGGTGCTTTGA  
 CATGGCGACCGGCCAGTTTGTGCTCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGC  
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTATC  
 CTGTACGCGCAGCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC  
 CTACGGGGACCGCGTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCA  
 ACGACTTCGACACCTACATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGAC**TGA**GGG  
 CCTCTGGGCCACCCCTCCCGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG  
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGA  
 CCCTGCTTCTATCTTGGCTGCCATCATCCCTCCCAGCCTATTTCTGCTCCTCTCTTCTCTCT  
 TGGACCTATTTTAAAGAGCTTGCTAACCTAAATATTCTAGAACTTTCCCAGCCTCGTAGCCC  
 AGCACTTCTCAAACCTTGGAAATGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCT  
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCTCTGGGTGATGCTG  
 ATGGGGTCAGTCTATGAACCACACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAG  
 TACTTTCTGAACATTCTGGAATCCTCCCCACATTCTAGAACTTCTCCCAACATTTTTTTTTCT  
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACTGC  
 AACCTCTGCCTCCCGGGTTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC  
 AGGCGCTGCTACCATGCCTGGCTAATTTTTGTATTTTATAGATAGAGATGGGGTTTACCATA  
 TTGGCCAGGCTGGTCTTGAACCTCCTGACTTCAGGTGACCCACCCGCCCTCGGCCTCTCAAAT  
 GCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCCAATTCCAACATTCTTAAATTCTCTCAT  
 CCCTCCAGGGCTCCCCGTGCTATGTTCTCTTTACCCCTTCCCCCTCTTCTCTTGCTCAGGCC  
 TGCACCACTGCAGCCACCGTTTCAATTATTATTATTAAACACTGAGCACTCACTCTGTGCT  
 GGGTCCCGGGAAGGGTGAGGGGGTCAGACACAGGCCCTGCCCTCAGTGACTGGCCA  
 GTCCAGCCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCATGGGG  
 GCCTGTGTTCTGGGTGTTTCAAGTGCTGCTGGTCCCTTACCCACTGCTCCCCAAGGCTGG  
 TGGGACGGGGTCCCGGTGGCAGGGGCAGGTATCTCCTTCCCGTTTCTCATCCACCTGCCAG  
 TGCTCATCGTTACAGCAAACCCAGGGGGCCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG  
 ACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGCCCCGAAGAATGGAACCCACACCCA  
 TAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAGACCTGCCCTCCTCACTGGGATCCC  
 CTTCTCTGCTCCTCCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAAGTCATCT  
 GAACTTCCGTTTCCCCAGGGCCTCCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCT  
 CTCTGCCCCCTCATGCCCCCTCTACCCGGCCAGTGCCCCGACTCTCCAGGCTTTATCAAGGTG  
 CTAAGGCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCCTCCTCCGGCCTGGTGCTGCCTTTAC  
 AAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG  
 AGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCGTTTCTTCTTCCAGGGTGGGGTGGCCTGGT  
 GTTCCCCCTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAGAGGGAGGGCCCTCCGC  
 CCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGGTGATCTCTGGTGCTCAC  
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGCCAGGA  
 AGACCTGTGCTATAAACACCCTGCCTGATCCTGCCCTGCCTGACCCCGCCACGCCCTGCC  
 GTCCAGCATGATTAAAGAATGCTGTCTCCTCTTGAAAAA

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## **FIGURE 30**

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH  
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPPGPQGSKGDKGEMGSPGAPCQKRF  
FAFSVGRKTALHSGEDFQTLLEFVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET  
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT  
FSGHLIKAEDD

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 72-75

#### **C1q domain proteins.**

amino acids 144-178, 78-111 and 84-117

**FIGURE 31**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGACCCGCCAGGAAAGACTG  
 AGGCCGCGGCCTGCCCCGCGGCTCCCTGCGCCGCGCGCCTCCCGGGACAGAAG**ATG**TG  
 CTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAGG  
 GCTGCCCATCCGGCTGCCAGTGCCAGCCAGCCACAGACAGTCTTCTGCACTGCCCCGCCAGGGG  
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT  
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCCTGGACCTGTAC  
 AGAACCAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTG  
 GACCTGACGGCCAACAGGCTGCATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCT  
 CGAGCGCCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC  
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCGCTGCGC  
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT  
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG  
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAG  
 CGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACAC  
 CCGCATTGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATG  
 TGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCGCTGCGG  
 CTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTG  
 GGTGCGCGAGAGCCACGTCACTAGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCA  
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACC  
 ACCACAGCCACAGTGCCACCACGAGGCCCCGTGGTGCGGGAGCCACAGCCTTGTCTTCTAG  
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCA  
 CTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC  
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTT  
 CACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCCAGCCCTACACCAGTCA  
 CGCCGAGGCCACCACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGC  
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA  
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG  
 AGTACACGGTCACCCAGCTGCGGCCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGG  
 CCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTGCGGGGAGGCCCATACCCCCAGCCGTCCA  
 CTCCAACCACGCCCCAGTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTTGCGCCG  
 CCCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACAGCCTACTGTGTGCGGCGG  
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCT  
 GGAAGTGGAGGGAGTGAAGTCCCCCTTGAGGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAG  
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTC  
 CAGTCACCCCTCCACGCAAAGCCCTACATCT**TAA**GCCAGAGAGAGACAGGGCAGCTGGGGCCG  
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCC  
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA  
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC  
 CGAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG  
 GGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA  
 CCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTG  
 TGAAGTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTA  
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG  
 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATG  
 AAGGCCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAAA

**FIGURE 32**

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDVPPDTVGLYVFEN  
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR  
RLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP  
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLVDVSDNQLERVPPVIRGLRGLTRLRLAG  
NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFG  
PWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS  
SSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGRHHLACLCPE  
GFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRL  
TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPA  
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGAAVCVRRGRAMAAAAQDKGQVGPAGAG  
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI



GAATCATCCACGACCTGCGAGCTCTGCTGAGAGAGTGCAGAGCCGTGGGGGTTTTTGAGACTCAT  
CTTCATCATTCATCATATGAGGAAATAAGTGGTAAAAATCCTTGGAAATACAATGAGACTCATCAG  
AAACATTTACATATTTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG  
AAGAAAGGGAAGTGTGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTGG  
ACCCAGCCACAACGACACTGGATTATCCTATAACCTCCTTTTTCAACTCCAGAGTTTCAGA  
TTTTCATTTCTGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAAATCAACAGCTGG  
ATCTCAAAAGCTTTGAATTCAAACAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTG  
AAGAGTGTAACCTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT  
TGACACCATGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA  
GTGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTCT  
TTCTTAGGATTCAGAACTCTTCCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAAC  
AAAACCTGCACATTGTTTTTACCAATGGACACAAATTTCTGGGTTCTTTGCGTGATGGAATCA  
AGACTTCAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA  
ATGCAACGAAATCTTAGTTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA  
TTTACTCTGGGACGACCTTTTCCTTATCTTACAATTTGTTTGGCATACATCAGTGGAACT  
TTCAGATCCGAAATGTGACTTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC  
TCAATACTGTAAATGAGAATATAAAATTTGGAGCATGACATTTAGAGTGTTTTACATTCA  
ACAGGATAAAATCTATTTGCTTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAATG  
CACAAATGCCACACATGCTTTTTCCGAATTATCCTACGAAATTCCAATATTTAAATTTTGGC  
AATAATATCTTAAACAGACGAGTTGTTTAAAGAAGTATCCAACCTGCCTCACTTGAAAACCTCT  
CATTTTGAATGGCAATAAACTGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACAC  
CCTTGGAACTTGGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAATTTGCTCA  
TGGCCAGAACTGTGGTCAATATGAATCTGTACATACAATAAATTTGCTGATTTCTGTCTTCAG  
TGCTTTGCCCAAAGTATTCAAATACTTGACCTAAATAATAACCAATCCAACCTGTACCTA  
AAGAGACTATTCATCTGATGGCCTTACGAGAACTAAATATTGCATTTAATTTTCTAACTGAT  
CTCCCTGGATGCAGTCATTTAGTAGACTTTAGTTCTGAACATTTGAAATGAACCTTCATTCT  
CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAAACCTTAAATGCGGGAAGAA  
ATCCATTCCGGTGACCTGTGAATTAATAAATTTTATTGAGTTGAAACATATTCAGAGGTC  
ATGATGTTGGATGGTCAGATTTACACACCTGTGAATACCTTTTAAACCTAAGGGGAAGTAG  
GTTAAAAGACGTTTATCTCCACGAATTATCTTGCAACACAGCTCTGTTGATTGTCACCATTTG  
TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCCC  
TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAACAAACCA  
AGAACAACCTCAAGAGAAATGTCCGATTTCCAGCATTTATTTTATACAGTGAACATGATTTCTC  
TGTGGGTGAAGAATGAATTTGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTTGC  
CTTTATGAAAGCTACTTTGACCCTGGCAAAAGCATTAGTGAAAATATTGTAAGCTTCATTGA  
GAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCAACTTTGTCCAGAATGAGTGGTGCCATT  
ATGAATTCTACTTTGCCCAACCAATCTCTTCCATGAAAATTTCTGATCATATAATTTCTATC  
TTACTGAAACCCATTTCATTCTATTGCATTTCCACAGGTATCATAACTGAAAGCTCTCCT  
GGAAAAAAGCATACTTTGGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCAA  
ACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCAGAGAAATGTATGAACTGCAGACA  
TTCACAGAGTTAAATGAAGAGTCTCGAGGTCTACAATCTCTCTGATGAGAACAGATTTGTCT  
ATAAATCCACAGTCCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTTGATA  
CAACCTTTATGATGGCAATTTGACAATATTTATTAATAAATAAATGTTATTTCCCTTCATA  
TCAGTTTCTAGAAAGGATTTCTAAGAATGTATTCCTATAGAAAACCTTCACAAGTTTATAAGG  
GCTTATGAAAAAAGGTGTTTATCTCCAGGATTTGTTATAATCATGAAAAATGTGGCCAGGTGC  
AGTGGCTCACTCTTGTAATCCAGCACTATGGGAGGCCAAGGTGGGTGACCCACGAGGTCAA  
GAGATGGAGACCATCCTGGCCAACATGGTGAAACCTGTCTCTACTAAAAATACAAAATTA  
GCTGGGCGTGATGGTGCACGCCTGTAGTCCAGCTACTTTGGGAGGCTGAGGCAGGAGATCG  
CTTGAACCCGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGGCTGCACTCCAGCCCTGGT  
GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGAAAAACATCC  
TCATGGCCACAAAAATAAGGTCTAATTCAATAAATTATAGTACATTAATGTAATATAATATTA  
CATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTGGTATGGAAAAACATATTAATAT  
GTTATAAATCTATTAGGTTGGTGCAAACTAATTGTGGTTTTTGGCATTTGAAATGGCATTTGAA  
ATAAAGTGTAAAGAAATCTATACAGATGTAGTACAGTGGTTGGGTCTGGGAGGTTGGA  
TTACAGGGGACATTTGATTTCTATGTTGTGTTATTTCTATAATGTTTGAATTGTTTAGAATGA  
ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

**FIGURE 34**

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ  
LQSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL  
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP  
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL  
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR  
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP  
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNDENC SWPETVVNMNLSYNKLS  
DSVFRCLPKSIQILD LNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGC SHFSRLSVLNIE  
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN  
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCC LHFDLPWYLRMLGQCTQTWHRV  
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI  
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHHNLFHENS DH IILILLEPIPFYCIPTRYHK  
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM  
RTDCL

**FIGURE 35**

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACACCTGCCTCCAAGGACCGGCCCTCGGAGGGGTGCGCGGAAAGG  
 GAGGGAAGAAGGAAGGGCGGGGCGGGCCCCCTGCGCCCGCCCCGCGCTCTGCGCGCCCCGTCCGCCCGGGC  
 CCAGCCCAGCCCCAGCCCCGCGGGCCGGTCAACAGCGCAGCCAGCCGGCCGCTCCCGCGCCCCAAGCGCGCCGCT  
 CTGCTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCCGCAGCCCCGCGGGCGCCCCGGTGACCGTGA  
 CCCTGCCCTGGGCGCGGGGCGGAGCAGGCATGTCCC GCCCGGGGACCGCTACCCAGCGCTGGCCCTGGTGCTC  
 CTGGCAGTGACCTGGCCGGGGTCTGGAGCCCAGGGCGCAGCCCTCGAGGACCCTGATTATTACGGGCAGGAGAT  
 CTGGAGCCGGGAGCCCTACTACGCGCGCCCCGAGCCCGAGCTCGAGACCTTCTCTCCGCCGCTGCCTGCGGGG  
 CCGGGGAGGAGTGGGAGCGGCGCCCCGAGGAGCCCGAGCCCGCCCCAAGAGGGCCACCAAGCCCCAAGAAAGCTCCC  
 AAGAGGGAGAAGTCCGCTCCGGAGCCGCTCCACCCAGGTAAACACAGCAACAAAAAAGTTATGAGAACCAAGAG  
 CTCTGAGAAGGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCCGTGAAGATGTCAGAGAGAGTTGCCACCTC  
 TTGGTCTGGAAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCCTGGGGGCA  
 CATCGAGGAGACTCAACATCCAGGCGGGCATTAAATGAAAATGATTTTTATGACGGAGCGTGGTGCGCGGGAAG  
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGGTGTCACTCAAGGGA  
 GGAATCCCTCTGGCTGAGTGACTGGGTGACATCCTATAAGGTGATGGTGAGCAATGACAGCCACACGTGGGT  
 ACTGTTAAGAATGGATCTGGAGACATGATATTTGAGGGAAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCT  
 ACCCGTCCCCATGGTGGCCCGCTACATCCGCATAAACCCCTCAGTCTGGTTTGATAATGGGAGCATCTGCATGA  
 GAATGGAGATCCTGGGCTGCCACTGCCAGATCCTAATAATTATTATCACCGCCGGAACGAGATGACCACCACT  
 GATGACCTGGATTTTAAGCACCACAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCC  
 CAATATCACCAGAATTTACAACATTGGAAAAAGCCACCAGGGCCTGAAGCTGTATGCTGTGGAGATCTCAGATC  
 ACCCTGGGGAGCATGAAGTCGGTGAGCCCCGAGTTCCACTACATCGCGGGGGGCCACGGAATGAGGTGCTGGG  
 CGGGAGCTGCTGCTGCTGGTGCAGTTCGTGTGTGAGGAGTACTTGGCCCCGAATGCGCGCATCGTCCACCT  
 GGTGGAGGAGACGCGGATTACGTCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCTACGAAGGGGGCT  
 CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTTCTGATTTA  
 AACACGCTGCTCTGGGAGGCGAGGATCGACAGAATGTCCCCAGGAAAGTTCCCAATCACTATATTGCAATCCC  
 TGAGTGGTTTCTGTGCGAAAATGCCACGGTGGCTGCCGAGACCAGAGCAGTCATAGCCTGGATGGAAAAATCC  
 CTTTTGTGCTGGGCGGCAACCTGCAGGGCGGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGCGGTCCCC  
 TGGAAGCGCAGGAACACACCCCCACCCCGATGACCACGTGTTCCGCTGGCTGGCCTACTCCTATGCCTCCAC  
 ACACCGCCTCATGACAGACGCCCGGAGGAGGGTGTGCCACACGGAGGACTTCCAGAAGGAGGAGGGCACTGTCA  
 ATGGGGCCTCCTGGCACACCGTGCCTGGAAGTCTGAACGATTTAGCTACCTTCATACAACTGCTTCGAATG  
 TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCCGAGGAGTGGGAGAATAACCGGGAATC  
 TCTGATCGTGTTCATGGAGCAGGTTTCATCGTGGCATTAAAGGCTTGGTGAGAGATTCATATGGAAAAGGAATCC  
 CAAACGCCATTATCTCCGTAGAAGGCATTAACCATGACATCGAACAGCCAACGATGGGGATTACTGGCGCTC  
 CTGAACCTGGAGAGTATGTGGTCACAGCAAAGGCCGAAGTTTCACTGCATCCACCAAGAACTGTATGGTTGG  
 CTATGACATGGGGGCCACAAGGTGTGACTTCACACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGG  
 AGAAGTTTGGGAAGCAGCCCGTCAGCCTGCCAGCCAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACAGCGT  
 GGGTGAACCTCCTGGGCCCTTGAGACTCGTCTGGGACCCATGCAAAATAAACCAACCTGGTAGTAGCTCCATAG  
 TGGACTCACTCACTGTTGTTTCTCTGTAATTCAAGAAGTGCCCTGGAAGAGAGGGTGCAATGTGAGGCAGGTCC  
 CAAAAGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTTCTTTGTTCCCATTTATCCAAATAACTTGGACAGAGCA  
 GCAGAGAAAAGCTGATGGGAGTGAGAGAACTCAGCAAGCCAACTGGGGAATCAGAGAGAGAAGGAGAAGGAGGG  
 GAGCCTGTCCGTTAGAGCCCTCTGGCTGCATAGAAAAGGATTCTGGTGCTTCCCCTGTTTGCGTGGCAGCAAGG  
 GTTCCACGTGCAATTTGCAATTTGCACAGCTAAAATTGCAGCATTTCAGCTGGGCTGTCCCAATGTTACCA  
 TTTGAGATGCTCCAGGCGTCTAAGAGAATCCACCCTCTCTGGCCCTGGGACATTGCAAGCTGCTACAAATAA  
 ATTCTGTGTTCTTTTGACAATAGCGTCATTGCCAAGTGCACATCAGTGAGCCTCTTGAATCTGTTTAGTCTCCT  
 TTTTCAACAAAGGAGTGTGTTTCAAGAAAGGAGAGAGAGGCTGAGATCATTACAGGAGTTTGTGGGCGAGCAAGCA  
 TGGAGCTTCTGCACAAATTTCTGGTCCATAAAACAACCCCCAAAGTCCCTGCTGATCCAGTAGCCCTGGAGGTT  
 CCCCAGGTAGGGAGAGCCAGAGGTGCCAGCCTTCTGAAGGGCCAGAAAATTTAGCCTGGATCTCCTCTTTTAC  
 CTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCCTGAAGCCCTCTCTGCTTGAGGTATTGCCCTGTGTG  
 GAATTGAGTGCTCATGGGTGGCCTCATATCAGCCTGGGAGTTATTTTTGATATGTAGAATGCCAGATCTTCCA  
 GATTAGGCTAAATGTAATGAAAACCTCTTAGGATTATCTGTGGAGCATCAGTTTGGGAAGAAATATTGAATTAT  
 CTTGCAAGAAAAAAGTATGTCTCACTTTTTGTAAATGTTGCTGCCTCATTGACCTGGGAAAAATGAAAAAAA  
 AATAAAGCAAATGGTAAGACCCTTAAAAA

**FIGURE 36**

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPPLP  
AGPGEEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS  
VRVAREDVRESCPPLGLETCLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA  
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF  
EGNSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT  
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF  
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG  
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA  
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYSAST  
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES  
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKIPNAIISVEGINHDIRTANDGDYWRL  
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARI REIMEKFGKQPVSLPARR  
LKLGRGRRRQRG

**FIGURE 37**

CTAAGAGGACAAG**ATG**AGGCCCGGCCTCTCATTTCTCCTAGCCCTTCTGTTCTTCCTTGGCCAAGCTGCAGGGG  
 ATTTGGGGGATGTGGGACCTCCAATTTCCAGCCCCGCTTCAGCTCTTTCCCAGGTGTTGACTCCAGCTCCAGC  
 TTCAGCTCCAGCTCCAGGTCGGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTTCTGTGTCCAGTTGTT  
 TTCCAATTTACCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACCACCTTTC  
 CCGTGGACAGAGTGAACGCTTGAATTCACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAGAACTTTCTAAA  
 GTGAGGGAATATGTCCAATTAATTAGTGTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATTGACATCAT  
 GGAGAAGGATACCAATTTCTTACACTGAACTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC  
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAAGCTCAGAAATTTGTTGACCAGCTGGAGGTGGAGATAAGAAAT  
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATGTCTTGCCATTGCGCGAGAAATCGTGGC  
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAAACACCCCTGTGTCACCCCTCCTCCCACTC  
 CAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGTGGTTTCAGCTCAACTGGAGAGGGTTT  
 TCTTATCTATATGGTGCTTGGGTAGGGATTACTCTCCCAGCATCCAAACAAAGGACTGTATTGGGTGGCGCC  
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTTGCTATTGTATATAA  
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC  
 ATGTACAACACCGGGAATATTGCCAGAGTTAACCTGACCACCAACACGATTGCTGTGACTCAAACCTCTCCCTAA  
 TGCTGCCATATAATAACCGCTTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG  
 GATTGTGGGTTATTTATTTCAACTGAAGCCAGCACTGGTAACATGGTGTATTAGTAACTCAATGACACCACACTT  
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCCTTCATGGTATGTGGGGTTCT  
 GTATGCCACCCGTACTATGAACACCAGAACAGAGAGATTTTTTACTATTATGACACAAACACAGGGAAAGAGG  
 GCAAACAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTTGACCAGAAA  
 CTTTATGTCTATAACGATGGTTACCTTCTGAATTATGATCTTTCTGTCTTGCGAAGCCCCAG**TAA**GCTGTTTA  
 GGAGTTAGGGTGAAAAGAGAAAATGTTTGTGAAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT  
 CTAAAAGTGTGTTCAATTTTGCAGCAATGTTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT  
 TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGCAATAAAGTCTGTCTAGGGTGGGA  
 TTGTCAGAGGTCTAGGGGCACTGTGGGCCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA  
 GGAATTAAGGAACTTAAACCTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAAATATTGCCAATGACTAGTC  
 CTCATCCATGTAGCACCCTAATCTTCCATGCCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCT  
 GGAGCTCCTCGAGGGACCAATCTCCAACTTTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG  
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAAGTGCTGAGTTTTATGGAGAGAGGCCTTTTT  
 ATGCATTAAATTTGACATGGCAAATAAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTTCTTTCTCTC  
 ATTGTCACCTTACTAAAAGTCAGTAGAATCTTCTACCTCATAACTTCCTTCCAAAGGCAGCTCAGAAGATTAG  
 AACCAGACTTACTAACCAATTCACCCCCCACCACCCCTTCTACTGCCTACTTTAAAAAAATTAATAGTTTT  
 CTATGGAAGTATCTAAGATTAGAAAAATTAATTTCTTTAATTTTCAATATGGACTTTTTATTTACATGACTCTA  
 AGACTATAAGAAAATCTGATGGCAGTGACAAAGTGCTAGCATTTATTGTTATCTAATAAAGACCTTGGAGCATA  
 TGTGCAACTTATGAGTGTATCAGTTGTTGCATGTAATTTTGCCTTTGTTAAGCCTGGAACCTGTAAGAAAAT  
 GAAAATTTAATTTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT  
 TGGAAACCTTGCTGGTGTATGTGATGTGCTTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT  
 TCCTTTGATGTTCAAGTCCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCCCTTTTAAAAATAAATGAT  
 TAAATGTGCTTTGAAAAA

**FIGURE 38**

MRPGLSFLLALLFFLGQAAGDLGDVGPPIPSPGFSSFPGVDSFFFSSSSSRSGSSSSRSLGS  
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV  
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ  
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTCLKECEASKDQNTPVVHPPPTPGSCGH  
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGLYWVAPLNTDGRLLLEYRLYNTLD  
DLLLYINARELRITYGQSGTAVYNNNNMYVNMVNTGNIARVNLTNTIAVTQTLNAAAYNNR  
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF  
MVCGLVLYATRTMNRTEEIIFYYYDTNTGKEGKLIVMHKMQEKVQSINYNPFDQKLYVYNDG  
YLLNYDLSVLQKPQ

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAACACCCCCTGTCGTCCAC  
CCTCCTCCCCTCCAGGGAGCTGTGGTTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT  
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC  
CCCAGCATCAAACAAAGGNATGTATTGGNGGCCATTGAATACAGATGGGAGACTGTTG  
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT  
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA  
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

TCTCGCAGATAGTAAATAATCTCTGGAAAGGCGAGAAAGAGCTGTCTCCATCTTGTCTGTAT  
CCGCTGCTCTTGTGTGACGTTGTGGAG**ATG**GGGAGCGTCTCTGGGGCTGTGCTCCATGGCGAGCT  
GGATACCATGTTTGTGTGGAAGTGCCCCGTGTTTGCTATGCCGATGCTGTCTTAGTGGAAC  
AACTCCACTGTAACTAGATTGATCTATGCACTTTTCTTGCTTGTGTGGAGTATGTGTAGCTTG  
TGTAATGTTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCTCGGATTTTGTGAGAATT  
AGAAAGGTGTTGTGCCCTTTGTAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT  
GGTTTGGCTATGTTCTATCTTCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA  
TCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTA  
TTATTGGGGCATTCTTCATTCCAGAAGGAACTTTACAACCTGTGTGGTTTTATGTAGGCATG  
GCAGGTGCCTTTTGTTTTCAATCCTCATACAACCTAGTCTTACTTATTGATTTTGCACATTCATG  
GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCGAGCCTTGT  
TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTGTTCTTTGTCTAC  
TACACTCATCCAGCCAGTTGTTTCAGAAAAACAAGGCGTTCATCAGTGTCAACATGCTCCTCTG  
CGTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTT  
TGTTACAGTCTTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGTATGACCAAT  
GAACCAGAAACAAATTGCAACCCCAAGTCTACTAAGCATAAATTGGCTACAATACAACAAGCAC  
TGTCCTCCAAAGGAAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTAATTC  
TCTTTTTTGTGTGTGTATTTTATTCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAA  
CTGACTCTAACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATC  
ACTGGAGGATGGGGACGATGTTTACCAGGCTGTAGATAATGAAAGGGATGGTGTCACTTACA  
GTTATTTCTTTCTTTTCACTTCACTGCTTTTCTGGCTTCACTTTAATATCATGATGACCCTTACC  
AAGTGGTCCAGGTATGAACCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA  
AATCTCTTCCAGTTGGATTGGCATCGTGTGTATGTTTGGACACTCGTGGCACCACCTTGTTT  
TTACAAATCGTGATTTTGACT**TGA**GTGAGACTTCTAGCATGAAAGTCCCACCTTTGATTATTGC  
TTATTTGAAAACAGTATTCCCAACTTTTGTAAGTTGTGTATGTTTGTGTTTCCCATGTAAC  
TTCTCCAGTGTTCTGGCATGAATTAGATTTTACTGCTTGTGCTATTTTGTATTTTCTTACCA  
GTGCATTGATATGTGAAGTAGAATGAATTGCAGAGGAAAGTTTTATGAATATGGTGATGAGT  
TAGTAAAAGTGGCCATTATTGGGCTTATTCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA  
ACAAATTTGTTTGACTATTTTAAAATTATATTAGACCTTAAGCTGTTTTAGCAAGCATTAAA  
GCAAAATGTATGGCTGCCTTTTGAATATTTGATGTGTGCTGGCAGGATAGTGCAAAAGAAC  
ATGGTTTATTTTAAATTTATAAACAAAGTCACTTAAATGCCAGTTGTCTGAAAAAATCTTATA  
AGTTTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGACAATAGTGTAGG  
TTATGGATGGAGGTGTGGTACTAAATTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA  
TGGCCTTTGCCAACAAAGTGAACCTGTTTTGGTTGTTTTAAACTCATGAAGTATGGGTTCAGT  
GGAAATGTTTTGAAGATCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGA  
AGGAAGTGTTTTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCAGCACGGTAGCTCACCCCTT  
GGTAATCCCAGCACTTTGGGAGCTTAAAGTGGGTAGATTACTTGAGCCCAGGAATTCAGACCA  
GCTTGGCACATGGTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCCTGTGGTC  
CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCAAGGCCAAAGGTTGCAGTGAGCAAGTCA  
CGTCACTGCACCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATTGAAATCAAGG  
AGGCAAAATTTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCCTTTAGTAGGTACTTAT  
ATAAAATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA  
GCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATAATAGCATTCTCTCTGACATTTAA  
AAATAATTTCTATTCAAAATACATGCATATTGATTTACACCTCATACTGTGATAATTAATGT  
GATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAAGAATGATGGAATGTTTT  
AGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAGATGTTTAAATGCTTTTGTAT  
TTACTGCCATGTAATTGAAATATATAGATTATTGTAACCTTTCAACCTGAAAATCAAGCAGT  
ATGAGAGTTTTAGTTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTACAATT  
TCTTCTTTAAAAATATTTATTAATGTGAATGGAATATAACAATTCAGCTTAAATCCCACAC  
TTATTTCTGTGTGATAGCAATTTGATTTCCAAATTTTGAATGGCTGTGTTTACCTCTAAATAA  
ATGAATTCAGAGAAAAA



**FIGURE 41**

MGSVLGGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME  
EQLNKIPGFCENEKGVVPCNILVGKYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG  
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM  
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSSENKAFISVNMLLCVGASVMSI  
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV  
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH  
RAVDNERDGVTSYSFFHFMFLASLYIMMTLTNWSRYEPSREMKSQWTAVVVKISSSWIGI  
VLYVWTLVAPLVLTNRDFD

CGCAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNACGTTGTGGAGAT  
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC  
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAACAANTCCACTGTAAGTAGATTGATCTA  
TGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG  
AACAACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT  
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT  
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT  
TTTGTTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

**FIGURE 43**

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC  
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNTATGCCGATGCTGTCCTAGTGGAACAANTCC  
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTTGGAGTANGTGTAGCTTGTGTAAT  
GTTGATACCAGGAATGGAAGAACAACGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG  
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG  
GCTANGTTCTATNTTCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG  
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG  
GGGC

**FIGURE 44**

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC  
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT  
TGCTATGCCGATGCTGTCCTAGTGGAAACAACCTCCACTGTAAGTAGATTGATCTATGCACTT  
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC  
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG  
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTA  
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT  
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

**FIGURE 45**

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACTTTTTCTTG  
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA  
AGATTCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC  
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT  
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT  
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT  
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACTAGT  
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA  
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA  
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC  
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

**FIGURE 46**

CTCGGGCGCGCACAGGCAGCTCGGTTTGGCCTGCGATTGAGCTGCGGGTCGCGGGCGGCGCGGCGCTCTCCAAT  
GGCAAATGTGTGTGGCTGGAGGCGAGCGGAGGCTTTTCGGCAAAGGCAGTCGAGTGTTCGAGACCGGGGCGAG  
TCCTGTGAAAGCAGATAAAAAGAAAACATTTATTAACGTGTATTACGAGGGGAGCGCCCGGCGGGGCTGTGCG  
ACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGCAGATTAC  
GTCGTTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTTATTAGCGATGCC  
CCCTGCTTTGTGTGTTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCC  
TGGGCGAATCCACATCTGTTTCAACTCTCCGCCGAGGGCGAGCAGGAGCGAGAGTGTGTGCAATCTGCGAGTG  
AAGAGGGACGAGGGGAAAAGAAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAAGAACACAGAT  
CAGCAAAAAAGAAAG**ATG**GGGCCCCCGAGCCTCGTGCTGTGCTTGTGTCCGCAACTGTGTTCTCCCTGCTGGG  
TGGAAGCTCGGCCTTCTGTGCGACCACCGCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCCA  
ACATCATCCTGGTGCTGACGGACGACCAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGCGCG  
ATCATGGAGCAGGGCGGGGCGCACTTCATCAACGCCTTCGTGACCACACCCATGTGCTGCCCTCACGCTCCTC  
CATCCTCACTGGCAAGTACGTCCACAACCAACACCTACACCAACAATGAGAAGTGTCTCGCCCTCCTGGC  
AGGCACAGCAGGAGAGCCGACCTTTGCCGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG  
TATCTTAATGAATACAACGGCTCCTACGTGCCACCCGGCTGGAAGGAGTGGGTGCGACTCCTTAAAACTCCCG  
CTTTTATAACTACAGCTGTGTGCGAACGGGGTGAAGAGAAGCACGGCTCCGACTACTCCAAGGATTACCTCA  
CAGACCTCATCACCATGACAGCGTGAGCTTCTCCGCACGTCCAAGAAGATGTACCCGCACAGGCCAGTCTCTC  
ATGGTCATCAGCCATGCAGCCCCCACGGCCCTGAGGATTCAGCCCCACAATATTCACGCCTCTTCCCAAACGC  
ATCTCAGCACATCACGCCGAGCTACAACTACGCGCCCAACCCGGACAAACACTGGATCATGCGCTACACGGGGC  
CCATGAAGCCCATCCACATGGAATTACCAACATGCTCCAGCGGAAGCGCTTGACAGCCCTCATGTGCGTGGAC  
GACTCCATGGAGACGATTTACAACATGCTGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACACCGC  
CGACCACGGTTACCACATCGGGCAAGCTTTGGCCTGGTGAAAGGGAAATCCATGCCATATGAGTTTGACATCAGGG  
TCCCCGTTCTACGTGAGGGGGCCCCAACGTGGAAGCCGGCTGTCTGAATCCCCACATCGTCTCAACATTGACCTG  
GCCCCACCATCCTGGACATTGCAGGCCTGGACATACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCT  
GGACACGAGCGCGCGGTGAATCGGTTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGGACTCCTTCTTGGTGG  
AGAGAGGCAAGCTGCTACACAAGAGAGACAATGACAAGGTGGACGCCCAGGAGGAGAACTTTCTGCCCAAGTAC  
CAGCGTGTGAAGGACCTGTGTCAGCGTGCTGAGTACCAGACGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTG  
TGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGCAAGGGCCCCATGCGGCTGGGCGGCAGCAGAGCCC  
TCTCCAACCTCGTGCCCAAGTACTACGGGCAGGGCAGCGAGGCCTGCACCTGTGACAGCGGGGACTACAAGCTC  
AGCCTGGCCGGACGCCGAAAAAACTCTTCAAGAAGAAGTACAAGGCCAGCTATGTCCGCAGTGCCTCCATCCG  
CTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCACGTAGGCCTGGGTGATGCCGCCAGCCCCGAAACCTCA  
CCAAGCGGCACTGGCCAGGGGCCCCCTGAGGACCAAGATGACAAGGATGGTGGGGACTTCAGTGGCATGGAGG  
CTTCCCAGTACTCAGCCGCCAACCCCATTAAGTGAACATCGGTGCTACATCCTAGAGAACGACACAGTCCA  
GTGTGACCTGGACCTGTACAAGTCCCTGCAGGCTGGAAAGACCACAAGCTGCACATCGACCACGAGATTGAAA  
CCCTGCAGAACAAAATTAAGAACCTGAGGGAAGTCCGAGGTACCTGAAGAAAAAGCGGCCAGAAAGATGTGAC  
TGTCACAAAATCAGTACCACACCAGCACAAAGGCCGCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTAG  
GAAGGGCCTGCAAGAGAAGGACAAGGTGTGGCTGTTGCGGGAGCAGAAGCGCAAGAAGAACTCCGCAAGCTGC  
TCAAGCGCCTGCAGAACACGACACGTGCAGCATGCCAGGCCTCAGTGTCTCACCCACGACAACACGACTGG  
CAGACGGCGCCTTTCTGGACACTGGGGCCTTTCTGTGCTGCACCAGCGCCAACAATAACACGTACTGGTGCAT  
GAGGACCATCAATGAGACTCACAATTTCTCTTCTGTGAATTTGCAACTGGCTTCCTAGAGTACTTTGATCTCA  
ACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACTGGACAGGGATGTCTCAACCAGCTACACGTACAG  
CTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGGACCTGGATGGAGG  
AAGCTATGAGCAATACAGGCAGTTTCAGCGTCGAAAGTGGCCAGAAATGAAGAGACCTTCTTCAAATCACTGG  
GACAACCTGTGGGAAGGCTGGGAAGGT**TAA**GAAACAACAGAGGTGGACCTCCAAAAACATAGAGGCATCACCTGA  
CTGCACAGGCAATGAAAAACCATGTGGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGGAGGCTGAGAAAAGC  
AAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCC  
ATTTTTGCCCCGTGCTTTTGGCTTTGGATTATACCTCACCAGCTGCACAAAATGCATTTTTTCGTATCAAAAAGTC  
ACCACTAACCTCCCCAGAGCTCACAAAGGAAAACGGAGAGAGCGAGCGAGAGAGATTTCTTGGAATTTTC  
TCCCAAGGGCGAAAGTCATTGGAATTTTAAATCATAGGGGAAAAGCAGTCCTGTTCTAAATCCTCTTATCTT  
TTGGTTTGTACAAAGAAGGAACTAAGAAGCAGGACAGAGGCAACGTGGAGAGGCTGAAAACAGTGCAGAGACG  
TTTGCAATGAGTCAGTAGCACAAAGAGATGACATTTACCTAGCACTATAAACCTGGTTGCTGTGAAGAAA  
CTGCTTCATTGTATATGTGACTATTTACATGTAATCAACATGGGAACTTTTAGGGGAACCTAATAAGAAAT  
CCCAATTTTCAGGAGTGGTGGTGTCAATAACGCTCTGTGGCAGTGTAAGAAAAA

**FIGURE 47**

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ  
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE  
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD  
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP  
SYNYAPNPDKHWMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT  
YIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI  
AGLDIPADM DGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN  
FLPKYQRVKDL CQRAEYQTACEQLGQKWQCVEDATGKLK LHKCKGPMRLGGSRALSNLVPKY  
YGQGSEACTCD SGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSV AIEVDGRVYHVGLGDAAQ  
PRNLTKRHWP GAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS  
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRLKHRGSSL  
HPFRKGLQEKDKVWLLREQKRKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG  
PFCACTSANNNTY WCMRTINETHNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL  
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

**FIGURE 48**

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA  
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC  
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCCTGCTGCTGCTGCTGCTGCTGGCCACC  
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA  
CCGAGTCCGCCGGGCCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC  
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC  
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA  
CGCTCGCTGAGGCTGCTGTGCGCCGGTGCCTGTGGACAGCAGCTGCCCCTGCCCTCCCATCTG  
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG  
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC  
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG  
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG  
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC  
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT  
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTCATCGGTGCCTTAGTCCAAGAAAAT  
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 49**

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRAPWPFR  
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

Figure 49

**FIGURE 50**

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCCATGTCGGACCTGCTA  
CTACTGGGCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG  
GTACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA  
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCTACTGAGAGC  
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC  
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC  
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC  
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG  
TGTCCATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG  
AGATCTACCAGGAAGACCAGATCCATTTTCTGTGCCCACTGGCACGGCAGGGAGACTTCTAT  
GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA  
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCC  
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGGGGCGAGCAGCCGTGGCTGGGAT  
GACGGTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA  
GGAGCTGGACTTGAGGGGCGAGGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC  
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAGTAACCC  
ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT  
CCAGCCCTCTTCCTCCTTCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC  
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA  
GGGACTATTTTCTGCACCAGCCCCCAGGGCTGCCGCCCTGTGTGTCTTTTTTTTTCAGACTC  
ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAA  
AAAAAAAAA

**FIGURE 51**

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR  
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRAVGSI LSEGEESPSPELIDLYQKFGFKVFS  
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHMCPLAR  
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS  
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK  
GKE

**FIGURE 52**

CCGCGGGAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT  
GCCCCGCGCCCAGTCATGACCCTGCGCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT  
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA  
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA  
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT  
GACCAGAGACCCTCTGGTTATAGA ACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA  
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT  
GGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT  
GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTGCTGCTGCTGCTGCT  
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT  
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAATA  
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 53**

MTLRPSLLPLHLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFCDTLHI  
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF  
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS  
KKKLKEEKRNKSKKK

**FIGURE 54**

CCCGGGAACGTGTTCTGGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC  
CCCGCGCCCAGTCATGACCCTGCGCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC  
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC  
CTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA  
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA  
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT  
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCCTTCTCACTTGGCCTATGG  
AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA  
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG  
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA  
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA  
AATAATAAATTTTAAAAAACTTA

**FIGURE 55**

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCC  
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG  
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA  
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT  
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT  
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG  
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC  
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA  
CAAGAGCAAAAAGAAATAATAATAATAAATTTAAAAAACTTAAAA

**FIGURE 56**

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGGAG  
TGAGGCGGGCCGGCGCGGGCGGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG  
ACCTGAAAAAA**ATG**TCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG  
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTTACAGGCTGGTGGAT  
TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATAACCATGCCT  
GTGGTGTATATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA  
GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTTGGCTTTTCGTTGG  
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTTGGAGGTTATGTTG  
CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTTCCAGAATGCCTTCATCTTT  
TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAG**TGA**ACACATCTGAT  
TTCCACAGCACAACAGCCCTGCATGGGTTTGTGTTTTTTTTACTGCTCACTCCCAACCTT  
TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT  
AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACTTGATTAACCT  
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT  
TGTA AAAAATAAAAAGAAATTACAAAAGAAATTATGGATTTGTCAATGTAAGTATTTGTCATA  
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT  
CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTTAGTTTTTTAAAATATTCCGTGG  
TCAA AATTCTTCCTCACTATAATTGGTATTTACTTTTACC AAAAATTCTGTGAACATGTAAT  
GTA ACTGGCTTTTGAGGGTCTCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT  
GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTCCGCTGTGCCTCTCATT  
CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC  
CACATCCACCACTG



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MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDA AVIYPTMKDFNHSYHACGVI  
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK  
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

TTCTTGGGCTAAATCGGGGGAGTGAGGCGGGCCGGCGCGGACACGGGGCTCCGGAACC  
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG  
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC  
TATTTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT  
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC  
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG  
CTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG  
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT  
TTTCCAGAATGCCTTCATCTTTTTTTGGAGGGCTGGTTTTTAAAGTTTGGC

**FIGURE 59**

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTTCAGAATGCATGAC  
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG  
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC  
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA  
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT  
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTTGGAGGT  
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC  
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

**FIGURE 60**

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT  
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT  
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT  
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC  
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGT  
GTTTGGGTCAAACAGGTGNTCGCATTGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT  
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT  
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

**FIGURE 61**

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC  
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT  
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC  
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG  
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN  
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC  
CCTGT

**FIGURE 62**

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG  
CGNGACACCGGGTTCCGGGAACCATTGACACGACGGGGTGGACTGACCTGAAAAAATGTTTG  
GATTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT  
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT  
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA  
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA  
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG  
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG  
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

**FIGURE 63**

CGACGCCGGCGT**GATG**TGGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGGCCGTCC  
TCTGCAAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC  
AAACGGCCCCCAGCGCCCCCTGGTAAGTACAAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC  
TTTTTTCAGCCAACCAAGTGCCGGAGAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG  
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCTCTGGTGTGGAACAACAT  
ACCAAGGCAGGGGGCTGCTGTCATACCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAAT  
CCATTACATTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTTATCTTGGACCAGATCACTG  
AAGGCGAGCTGGACTGGGCTCCCCCTGTCTCTCCTTTTGACATCATGGTACTGGAAGGGCCC  
AATGGCCGAAAGGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTACAGGGCCTCAAGGA  
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA  
GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTGCCCGTGGTTACAGTCTCTCGAC  
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCCCTTCAAGCATCCACCCAGAGCTTGGTGA  
GGTCTCGCAGCAGCTGGGGGCCTCCTCTGAGCTCCAGGCAGTACTCAGTACATCTTCCCCA  
CTTACGGTGTCAACCCCCAACACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTAC  
ATGAAAGGAGGCTTTTATCCCCGAGGGGGTTCCAGTGAAATTGCCTTCCACACCATCCCTGT  
GATTACAGCGGGCTGGGGGCGCTGTCTCACAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT  
CAGCTGGGAAAGCCTGTGGTGTGCTAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTGC  
CCCATCGTGGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC  
CCGCTGCCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGCGGCCCCGGCTTAGGCATGACCT  
CTGTTTTTCTATCTGCCTGCGAGGCACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTAT  
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGCTACGTCTCCATGCCCAGGGAAGA  
GGCTGCGGAACACATCCCTCTTCTCTTCTTCGCTTTCCCATCAGCCAAAGATCCGACCTGGG  
AGGACCGATTCCCAGGCGGTCACCATGATCATGCTCATACCCACTGCCTACGAGTGGTTT  
GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCAGTGAATGAGACCTTCAAAAACCTC  
CTTTGTGGAAGCCTCTATGTGCTAGTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGG  
AGAGTGTGACTGCAGGATCCCCACTCACCACAGTTCATCTGGCTGCTCCCCGAGGTGCC  
TGCTACGGGGCTGACCATGACCTGGGCGCCTGCACCCTTGTGTGATGGCCTCCTTGAGGGC  
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTGTGGACTGGTTCG  
GGGCCCTGCAAGGTGCCCTGCTGTGTCAGCAGCGCCATCCTGAAGCGGAACCTGTACTCAGAC  
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAAT**TAG**TTCCATCAGGGAGG  
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG  
CATTAGTTCCTTGACGTATAAAGCACTCTAATTGGTTCTGATGCCTGAAGAGAGGCCTAG  
TTTAAATCACAAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA  
TCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG  
TCTCATGACGAGCGGCGCTCTGCATCCCTCACCATGCCTCCTAACTCAGTGATCAAAGCGA  
ATATTCCATCTGTGGATAGAACCCTGGCAGTGTGTGTCAGCTCAACCTGGTGGGTTCAGTTC  
TGTCCTGAGGCTTCTGCTCTCATTTAGTGTACGCTGCACAGTTCTACACTGTCAAGG  
GAAAAGGGAGACTAATGAGGCTTAACTCAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA  
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTTCAAGTGGCTCTTCAGGGGACAGGAAAT  
GCCTGTGTCTGGCCAGTGTGGTCTTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA  
GGGTGCATGTGAGATGATCATATCCAATTATATGGAAGTCCCGGGTCTGTCTTCTTATCA  
TCGGGGTGGCAGCTGGTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGC  
CTTATCCACCAAATACACAGGGAAGGTGATGCAGGGAAGGGTGACATCAGGAGTCAGGGCA  
TGGACTGGTAAGATGAATACTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCCAGCCAAGGG  
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAGTCACATCAGAAAAGGGA  
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCATTTGCAGTTAATTAGCACATGTGAGGG  
TTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTTCAGTTATGTCTTTG  
GTATCAGACATACGAAAGGTCTCTTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATG  
ATTCCATTGCTTTAAAAA

**FIGURE 64**

MWLPLVLLLAVALLLAVLCKVYLGLEFSGSSPNPFSEDEVKRPPAPLVTDKEARKKVLKQAFSAN  
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG  
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQ  
EEAIIIDKYIKLVKVVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ  
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA  
GGAVLTKATVQSVLLDSAGKACGVSVKKGHELNIYCPIVVSNAGLFNTYEHLLPGNARCLP  
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYYDTDMDQAMERYVSMPREEAAEH  
IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAELKGKRGSDYETFKNSFVEA  
SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI  
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN



**FIGURE 65**

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA  
GGGGTTGGCACCGGCCCGAGAGGAGG**ATG**CGGGTCCGGATAGGGCTGACGCTGCTGCTGTG  
TGCGGTGCTGCTGAGCTTGGCCTCGGCGTCTCGGATGAAGAAGGCAGCCAGGATGAATCCT  
TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA  
GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGAATTAGAATCCTCTATTCAAGA  
AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG  
AGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAAACCAGCTTTG  
ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTTCTTAGATAA  
GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT  
ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAAACTGAAGAAGAGGCTGCTAAGAGA  
CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA  
TAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTGATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATC  
CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCAAGGGACAGACTGC  
TCTTGGCTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAAGGCTCTTGAT  
ATTATACATTTGGAGCTCTTGGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTT  
**TAG**TGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTTT  
TCAGCTTTCATGATCCAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACTTCCTTCAA  
ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACA  
ATTTTTCTTTAAATGATTAGTTTGGCTGATTGCCCCATAAAAGAGAGATCTGATAAATGGC  
TCTTTTAAATTTTCTCTGAGTTGGAATTGTCAGAATCATTTTTTACATTAGATTATCATAA  
TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAATGGTGGCTATAGAAAAACAACAT  
GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT  
GTGCAGAAATGACTCCAGAGAGCTCTACTTTCTGTTTTTTACTTTTCATGATTGGCTGTCTTC  
CCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCTTCCAGTAGTCTCATTTTCC  
CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACATTTTTTAATAAA  
ATTATGTCTAAGATTAAAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLDSKTTLTSDESVKDHTTAGRVVAGQIFLD  
SEESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG  
EPCHFPPFLFLDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMQEAEMM  
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMF EK  
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

**FIGURE 67**

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT  
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT  
GTCAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG  
CTCAACTCTCCTGCACGCTCAGCCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCCTGG  
TACCAGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA  
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCT  
GTGTCCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC  
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT  
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGG  
TTAATAATATTCAACATGTCAACAAC

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**FIGURE 68**

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG  
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

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CCGCCCCCGCCCCAGACACCGGCGCCGGGGCGCGGGGGCGCGGGGATGCGGCGCCCGGGGGCGG  
CGATGACCGCGGAGCGCACGCGCGGGGCCCGCCCTGACCCCGCCGCCCGCCCGCTGAGCCC  
CCCGCCGAGGTCCGGACAGGCCGAGATGACGCGCGAGCCCCCTGTTGCTGCTCCTGCTGCCCG  
CGCTGCTGCTGGGGGCCCTTCCCACCGGCCGCCGCCGCCGAGGCCCCCCCAAAGATGGCGGAC  
AAGGTGGTCCCACGCGCAGGTGGCCCCGGCTGGCGCGCACTGTGCGGCTGCAGTGCCAGTGGA  
GGGGACCCCGCCGCGCTGACCATGTGGACCAAGGATGGCGCACCATCCACAGCGGCTGGA  
GCCGCTTCCGCGTGCTGCCGCAAGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGGC  
GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCCCTCGTCGT  
GCTGGATGACATTAGCCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCCTCTGGGGGTCAAG  
AGGACCCCGCCAGCCAGCAGTGGGACGACCGCGCTTCACACAGCCCTCCAAGATGAGGCGC  
CGGGTGATCGCACGGCCCCGTGGGTAGCTCCGTGCGGCTCAAGTGCGTGGCCAGCGGGCACCC  
TCGGCCCGACATACGTGGATGAAGGACGACGAGCCTTGACGCGCCAGAGGCCGCTGAGC  
CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGAGGACAGCGGCAAATAC  
ACCTGCCGCGTGTGCAACCGCGCGGGCGCCATCAACGCCACCTACAAGGTGGATGTGATCCA  
GCGGACCCGTTCCAAGCCCGTGCTCACAGGCACGCACCCCGTGAACACGACGGTGGACTTCG  
GGGGGACCACGTCTTCCAGTGCAAGGTGCGCAGCGACGTGAAGCCGGTGATCCAGTGGCTG  
AAGCGCTGGAGTACGGCGCCGAGGGCCGCCACAACCTCACCATCGATGTGGGCGGCCAGAA  
GTTTGTGGTGCTGCCACGGGTGACGTGTGGTTCGCGGCCCGACGGCTCCTACCTCAATAAGC  
TGCTCATCACCCGTGCCCGCCAGGACGATGCGGGCATGTACATCTGCCTTGGCGCCAACACC  
ATGGGCTACAGCTTCCGCAGCGCCTTCTCACCCTGCTGCCAGACCCAAAACCCAGGGGCC  
ACCTGTGGCCTCCTCGTCTCCTCGGCCACTAGCCTGCCGTGGCCGTGGTATCGGCATCCCGAG  
CCGGCGCTGTCTTATCCTTGGGACCCCTGCTCTGTGGCTTTGCGAGGCCCCAGAAGAAGCCG  
TGCACCCCGCGCCTGCCCTCCCCCTGCCCTGGGACCCGCCCGCCGGGGACGGCCCGCGACCG  
CAGCGGAGACAAGGACCTTCCCTCGTTGGCCGCCCTCAGCGCTGGCCCTGGTGTGGGGCTGT  
GTGAGGAGCATGGGTCTCCGGCAGCCCCCAGCACTTACTGGGCCCAGGCCCAGTTGCTGGC  
CCTAAGTTGTACCCCAAACCTACACAGACATCCACACACACACACACACACTCTCACAC  
ACACTCACACGTGGAGGGCAAGGTCCACCAGCACATCCACTATCAGTGCTAGACGGCACCGT  
ATCTGCAGTGGGCACGGGGGGGGCCGGCCAGACAGGCAGACTGGGAGGATGGAGGACGGAGCT  
CGACAGCAAGGCAGGGGACCCATGGCGAGGAGGAATGGCCAGCACCCCGAGGCAGTCTGTGTG  
TGAGGCATAGCCCCTGACACACACACACAGACACACACACTACCTGGATGCATGTATGCAC  
ACACATGCGCGCACACGTGCTCCCTGAAGGCACACGTACGCACACGCACATGCACAGATATG  
CCGCCTGGGCACACAGATAAGCTGCCCAAATGCACGCACACGCACAGACATGCCAGATAA  
TACAAGGACATGCTGCCTGAACATACACACGCACACCCATGCGCAGATGTGCTGCCTGGACA  
CACACACACACACGGATATGCTGTCTGGACGCACACACGTGCAGATATGGTATCCGGACACA  
CACGTGCACAGATATGCTGCCTGGACACACAGATAATGCTGCCTTGACACACACATGCACGG  
ATATTGCCTGGACACACACACACACACACGCGTGCACAGATATGCTGTCTGGACACGCACAC  
ACATGCAGATATGCTGCCTGGACACACACTTCCAGACACACGTGCACAGCGCAGATATGCT  
GCCTGGACACACGCAGATATGCTGTCTAGTCACACACACACGCAGACATGCTGTCCGGACAC  
ACACACGCATGCACAGATATGCTGTCCGGACACACACACGCACGCAGATATGCTGCCTGGAC  
ACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGATATTGCCTGGACACACACA  
TGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATATGCTGTCCGGATACACACG  
CACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGACACACATGCACACACAGGT  
GCAGATATGCTGCCTGGACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGA  
TATTGCCTGGACACACACATGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATA  
TGCTGTCCGGATACACACGCACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGA  
CACACATGCACACACAGGTGCAGATATGCTGCCTGGACACACGCAGACTGACGCTGCTTTGG  
GAGGGTGTGCCGTGAAGCCTGCAGTACGTGTGCCGTGAGGCTCATAGTTGATGAGGGACCTTT  
CCCTGCTCCACCGTCACTCCCCCAACTCTGCCCGCCTCTGTCCCCGCCTCAGTCCCCGCCTC  
CATCCCCGCCTCTGTCCCCTGGCCTTGGCGGCTATTTTTTGCACCTGCCTTGGGTGCCCAGG  
AGTCCCCCTACTGCTGTGGGCTGGGGTTGGGGGCACAGCAGCCCCAAGCCTGAGAGGCTGGAG  
CCCATGGCTAGTGGCTCATCCCCAGTGCATTCTCCCCCTGACACAGAGAAGGGGCCCTTGGTA  
TTTATATTTAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTGCAGGGAC  
TGTGGTCTCTCTGGGGCCCGGGACCCGCGCTTTCAGCCATGCTGATGACCACCCCC  
GTCCAGGCCAGACACACCCCCCCCCACTGTGCTGGTGGCCCCAGATCTCTGTAATTTTA  
TGTAAGTTTGAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAAA

**FIGURE 70**

MTPSPLLLLLLPLLLLGAFPPAAAARGPPKMADKVVPQVARLGRTVRLQCPVEGDPPPLTM  
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK  
ESLGPDSSSSGGQEDPASQQWARPRFTQPSKMRRRVIAFPVGSSVRLKCVASGHPRPDITWMK  
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPV  
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD  
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA  
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS  
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHHTSHHVEGKV  
HQHIHYQC

**FIGURE 71**

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATTCAGAGTCA  
 AGTGACTCTGTGAAGCACCCACATCTACCTCTTGCCACGTTCCCACGGGCTTGGGGGAAAGATGGTGGGGACCA  
 AGGCCTGGGTGTTCTCCTTCCCTGGTCTGGAAGTCACATCTGTGTTGGGGAGACAGACGATGCTCACCCAGTCA  
 GTAAGAAGAGTCCAGCCTGGGAAGAAGAACCCAGCATCTTTGCCAAGCCTGCCGACACCCCTGGAGAGCCCTGG  
 TGAGTGGACAACATGGTTCAACATCGACTACCCAGGCGGGGAAGGGCGACTATGAGCGGCTGGACGCCATTCGCT  
 TCTACTATGGGGACCGTGTATGTGCCCGTCCCCTGCGGCTAGAGGCTCGGACCACTGACTGGACACCTGCGGGC  
 AGCACTGGCCAGGTGGTCCATGGTAGTCCCCGTGAGGGTTTCTGGTGCCTCAACAGGGAGCAGCGGCCCTGGCCA  
 GAACTGCTCTAATTACACCGTACGCTTCTCTGCCCCACAGGATCCCTGCGCCGAGACACAGAGCGCATCTGGA  
 GCCCATGGTCTCCCTGGAGCAAGTGCTCAGCTGCCTGTGGTCACTGAGGCTCCAGACTCGCACACGCAATTTGC  
 TTGGCAGAGATGGTGTGCTGTGCACTGAGGCCAGCGAAGAGGGTCACTGATGGCCAGGACTGTACAGC  
 CTGTGACCTGACCTGCCAATGGGCCAGGTGGCTGTTAAGACTTGTGAGGCGAGCAGGATAATGGGATCATGCTTC  
 ATGGGGCTGTCTCCCTTCCCGAGGTGCCCGAGCCTCAGGGGCTGCTATCTACCTCCTGACCAAGACGCCGAAG  
 CTGCTGACCCAGACAGCAGTGTATGGGAGATTCCGAATCCCTGGCTTGTGCCCTGATGGCAAAAGCATCTTGAA  
 GATCACAAAGGTCAAGTTTGCCCCATTGTACTACAATGCCAAGACTAGCCTGAAGGCAGCCACCATCAAGG  
 CAGAGTTTGTGAGGGCAGAGACTCCATACATGGTGTATGAACCTTGAGACAAAAGCACGGAGAGCTGGGCAGAGC  
 GTGTCTCTGTGCTGTAAAGCCACAGGGAAGCCAGGCCAGACAAGTATTTTGGTATCATAATGACACATTTGCT  
 GGATCTCTCCCTTACAGCATGAGAGCAAGCTGGTGTGAGGAACTGCAGCAGCAGCCAGGCTGGGGAGTACT  
 TTTGCAAGGCCAGAGTGTGCTGGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGTACAGCATCTGATGAG  
 ACTCCTTGAACCCAGTTCTCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTGAGATGCCACCACTC  
 TTTACTATAGCTGGGACGCTGCCCTGTTAAGACTTGTGAGGGCAGCAGGATAATGGGATCAGGTGCCGTG  
 ATGCTGTGCAAGTGTGTGGCATCTCCAAGACAGAGGAAGGGAGATCCAGTGCAGTGGCTACACGCTACCC  
 ACCAAGGTGGCCAAAGGAGTGCAGTGCAGCGGTGTACGGAACTCGGAGCATCGTGGGGGCCGTGTGCTGCT  
 TGCTGACAATGGGGAGCCCATGCGCTTTGGCCATGTGTACATGGGGAACAGCCGTGTAAGCATGACTGGCTACA  
 AGGGCACTTTACCCTCCATGTCCCCAGGACACTGAGAGGCTGGTGTACATTTGTGGACAGGCTGCAGAAG  
 TTTGTCAACACCACCAAGTGTACCTTTCAACAAGAGGGGAGTGGCGTGTCCATGAAATCAAGATGCTTCG  
 TCGGAAAGAGCCCATCACTTTGGAAGCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGGTGGTGAAGACC  
 CCATGGCTGAAGTGGAGATTCCATCCAGGAGTTTCTACAGGCAGAATGGGGAGCCCTACATAGGAAAAGTGAAG  
 GCCAGTGTGACCTTCTTGGATCCCCGGAATATTTCCACAGCCACAGCTGCCAGACTGACCTGAACCTTCACAA  
 TGACGAAGGAGACACTTTCCCCCTTGGACGTATGGCATGTTCTCTGTGGACTTCAGAGATGAGGTACCTCAG  
 AGCCACTTAATGCTGGCAAAGTGAAGGTCCACCTTGACTCGACCCAGGTCAAGATGCCAGAGCACATCCACA  
 GTGAAACTCTGGTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAAGGTGATTTCAAATTTGAAAATCAAAG  
 GAGGAACAAAAGAGAAGACAGAAGCTTCTGGTGGGCAACCTGGAGATTCTGTGAGAGGCTCTTTAACCTGG  
 ATGTTCTGAAAGCAGGCGGTGCTTTGTTAAGGTGAGGGCCTACCGGAGTGAGAGGTTCTTGCCTAGTGAGCAG  
 ATCCAGGGGTTGTGATCTCCGTGATTAACCTGGAGCCTAGAAGTGGCTTCTTGTCCAACCTAGGCTGGGG  
 CGCGTTTGACAGTGTCTACAGAGCCCAAGCGGCTGTGTGCTGCTTCTGTGATGACCACTCCCCTGATG  
 CCTACTCTGCCTATGTCTTGGCAAGCCTGGCTGGGGAGGAAGTGAAGCAGTGGAGTCTTCTCTAAATTCAC  
 CCAATGCAATTTGGCGTCCCTCAGCCCTATCTCAACAAGCTCAACTACCGTGGACGGACCATGAGGATCCACG  
 GGTAAAAAGACAGCTTTCCAGATTAGCATGGCCAGGCCAAGGCCAAGTCAAGTGGAGGAGCAATGGGCCCA  
 TCTATGCCTTTGAGAACCTCCGGGCATGTGAAGAGGCAACCCAGTGCAGCCCACTTCCGGTTCTACAGATT  
 GAGGGGGATCGATATGACTACAAACACAGTCCCCCTTCAACGAAGATGACCTATGAGTGGAGTGAAGATTGTGGGGCCACTGGAAGTGA  
 ATGTGCGATCCCGCAACATGGGGGGCACTCATCGCGGACAGTGGGGAAGCTGTATGGAATCCGAGATGTGAGG  
 AGCACTCGGGACAGGGACAGCCCAATGTCTCAGCTGCCTGTCTGGAGTTCAAGTGCAGTGGGATGCTCTATGA  
 TCAGGACCGTGTGGACCGCACCCCTGGTGAAGGTGATCCCCAGGCGAGTGCCTGCGAGCCAGTGTGAACCCCA  
 TGCTGCATGAGTACCTGGTCAACCACTTGCCACTTGCACTGCAACAACGACACCAAGTGAAGTACACCATGTGGCA  
 CCTTGGACCACTGGGCCACAATATGGCATCTACACTGTCACTGACCAAGGACCCCTGCAACAGCCCTGATCAACTAAAGTTTGTGGT  
 CGCGCTCGGCGGCTGCTTTGATGGCACATCCGATGGCTCCTCCAGAATCATGAAGAGCAATGTGGGAGTAGCCC  
 TCACCTTCAACTGTGTAGAGAGGCAAGTAGGCCGCCAGAGTGCCTTCCAGTACCTCCAAAGCACCCAGCCAG  
 TCCCCTGCTGCAGGCACTGTCCAAGGAAGAGTGCCCTCGAGGAGGACAGCAGCGAGCAGGGGTGGCCAGCG  
 CCAGGGTGGAGTGGTGGCCTCTCTGAGATTTCCTAGAGTTGCTCAACAGCCCTGATCAACTAAAGTTTGTGGT  
 ACTTCAACCTCTTCTGCCCTCATTTTATGTGACAGCCATTGTGAGACTGATGCACAACTGTCACTTGGTTAAT  
 TTAAGCACTTCTGTTTTCGTGAATTTGCTTGTGTTTCTTCTATGCCTTTACTTACTTTGTCCATGCTACTGA  
 TTGGCACGTGGCCCCACAATGGCACAAATAAAGCCCTTTGTGAAACTGTTCTTTAAATGAAACACAAGAAATT  
 GGCCACTGGTAAACTCTGCAGCTTCAACTGTACTTCAATTAATGCCATTAATGCAATATACTTCTCTTCTT  
 TTTGCATGGTTTGGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAAATAACCAATATAAAGCATAT  
 TTCTTGGCTTGTCTCCACAGGACATAGGCAAGCCTTGATCATAGTTTATACATATAAATGGTGGTGAATAAAG  
 AAATAAAACACAATACTTTTACTTGAAATGAAATAACTTATTTATTTCTTTGCTAAATTTGGAATTTAGTGG  
 ACATTCAAAGTTAAGCTATTAATAATAGGGTGATCATAGTTCTCTACCAAGTCTGGAAAGAACATCTCCTGGT  
 ATCCACAATTACACCAGGTTGCTAACTGTATTTGACATTTCCCTTGCATTCGCTTTTGTCTTGTAGAAAC  
 CCAGTGTAGCCAGGGCAGATGTCAATAAATGCATACTCTGTATTTGAAAAA

**FIGURE 72**

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI  
DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGS PREGFWCLNREQ  
RPGQNC SNYTVRFLCPPGSLRRDTERIWS PWS PWSKCSAACGQTGVQTRTRICLAEMVSLCS  
EASEEGQHCMGQDCTACDLTC PMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK  
TPKLLTQTDS DGRFRIPGLCPDGKSILKITKVKFAPIVL TMPKTS LKAATIKAEFVRAETPY  
MVMNPETKARRAGQSVSLCCKATGKPRPD KYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAG  
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQ NATNSFY YDVGRCPV  
KTCAGQQDNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRV  
SAADNGEPMRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLTFVDRLQKFVN TTKVLPFN  
KKGS AVFHEIKMLRRKEPIT LEAMETNII PLGEVVGEDPMAELEIPSR SFYRQNGEPYIGKV  
KASVTFLDPRNISTATAAQTD LNFINDEGDTFPLRTYGMFSVD FRDEVTSEPLNAGKVKVHL  
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL  
DVPESRRCFVKVRAYRSE RFLPSEQIQGVVISVINLEPRTGF LSNPRAWGRFDSVITGPNGA  
CVPAFCDDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPR  
VKKTAFQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTVPFN  
EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVR SRNMGGTHRRTVGKLYGIRDVRS  
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGS CRRASVNPMLHEYLVNHLPLAV  
NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT  
FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFP RVA  
QQPLIN



CTGCAAGTTGTTTAAACGCCCTAAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC  
AATATCTTAACTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG  
ACCTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACTAGACAAAGATCGCAGATCATAAAGC  
AAGCTCTGCTTTAGTTTTCCAAGAAGATTACAAAGAATTTAGAGATGTATTGTCAAGATCCCTGTGATTTCATG  
CCCTTTGGGTTACCGGTGTCCTCAGTGATGCAGCCCTACCCTTTGGTTTTGGGGAGCTATTGATTTGTGTAAGACT  
CAGATTTTACACGGAAGAAGGGAAGTTTGGGATTTACATGGCCTGCCAGCGGAATCCACGGACATGACAAAATA  
TCTGAAAGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCCTCCTGAGACGTTCTGTGCAATGGGCAATC  
CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGATTTT  
GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAAGGAGTATCCCAAGCCTCTCCAGGTTAAACAT  
CACTCTGTCTTGGAGCAAAACCATTGTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCGACAC  
AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA  
GATGCTTTTTACATGGATCCTAAATCCGTGAAGGATTTATCACAGCATACGGTCTTAGAAATCATTGTCACAGA  
AGAGTACTCAACAGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTGCGGCTTTTTTG  
CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAAACTCAGAGATTTCTTT  
ACAGTCACAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGC  
ACGCTACTTTTTACCGCATCTCAGACATAAAGTGCAGGAGGAGGTGCAAGTGTAATCTCCATGCCACTGTATGTG  
TGTATGACAACACGCAAAATGACATGCGAATGTGAGCAACAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAG  
AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCACTGCAAATACCTGTATCCC  
CAGTATTTCCAGTATTGGTACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGACGTGCCACA  
ACAACGTGCGCTGCCTGTGCCCGGCCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC  
AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCCGCACGGCACCCCGACGCTGCTGCTGACCACGCTGCT  
GGGAAACCCCGACCCCTTGGTGTCTTAGGTCTCACTCCAGCCACACCGACGGGCGCTGTGCCGTGGGGAAGCA  
GACACAACCCAAACATTTGCTACTAACATAGGAAAACACACATACAGACACCCCCACTCAGACAGTGTACAAA  
CTAAGAAGGCCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTCT  
TGACTCCAGAGGAGTTGGCAGCTGTTGATATTACTGCAATCACATTGCCAGCTGCAGAGCATATTGTGGA  
TTGGAAAGGCTGCGACAGCCCCCAAACAGGAAAGACAAAAACAACAAATCAACCGACCTAAAAACATTGGC  
TACTCTAGCGTGGTGCGCCCTAGTACGACTCCGCCAGTGTGTGGAACCAACCAATAGCATTCTTTGCTGTGAG  
GTGCATTGTGGGCATAAGGAAATCTGTTACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC  
CTGTGCTTTAGTGAACGTTGCTCTGTAACCCTCGTTGGTTGAAAGATTTCTTGTCTGATGTTAGTGATGCACA  
TGTGTAACAGCCCCCTCTAAAAGCGCAAGCCAGTCATACCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGGA  
GCACACCCCACTATACAAGAGTGGCTATAGGAAAAAAGAAAGTGATCTATCCTTTGTATTCAAATGAAGTT  
ATTTTCTTTGAACTACTGTAATATGTAGATTTTTTGATATTGCAATTTGTGTACCAGACAATCTGTTAAT  
GTATCTAATTGCAATCAAGACAAGACTGACATTTTATTTTGTCTCTTTCGTTCTGTTTTGTTTCACTGTGCAGA  
GATTTCTCTGTAAGGGCAACGAACGTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGTGTAAATAAGA  
TTCCACCAAAGGACATTCTAAATGTTTTCTTGTGTGCTTTAACACTGGAAGATTTAAAGAATAAAAACTCCTGCA  
TAAACGATTTCAGGAATTTGTATTGCAATTTCTTAAGATGAAAGGAACAGCCACCAAGCATTTACACTCACT  
TTACTGATTTCTGTGTGGACTGAGTACATTCAGCTGACGAATTTAGTTCAGGAAGATGATTGATGTTCACT  
AGCTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAAA  
AAAAAA

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**FIGURE 74**

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK  
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPPELMFDFEGRHPSTFWQSATWK  
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF  
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD  
TTKKLRDFFTVDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN  
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGTANTCIPSISSIGTNVCDNELLH  
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS  
PLVF

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**FIGURE 75**

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGGCGG  
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCCTCATGACTT  
CTCTTGTGGACCATGTCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC  
CCTCTCAGCCTCTACTGATTTTTTACCACACCCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA  
AGAGTTTAGCCTTGCGACTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT  
AGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC  
AGCAGCCATGGCCTTCTGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCTATGACA  
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTGAG  
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGAAAAAAT  
TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA  
ATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA  
CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT  
CATTTCGAGGAGTTCACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT  
TGGACCAAACCTCGTGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT  
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA  
AAAGGGCATGTCAGTGAAATCTGGGAATGGCTGGATTTCGGAACATCTGCCCATGTGTATTG  
ATGGCAGAGCTGTTGCCACAAGCGCCTTTTATTTAGGGTAAAATTAACAAATCCATTCTAT  
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCTTACATTTATATGATTCTGGGGTT  
GCTTCAGAAGTGTTATTTTCATGAATCATTATATGATTTGATCCCCCAGGATTCTATTTTGT  
TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAACCAT  
TTACTTTACATATTTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT  
TTGTAACAATAAATATTTTGGAGTAAATAATGGGTACATTTTAACAAACTCAGTAGTACAACC  
TAAACTTGATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAAATG  
AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAAAAA  
AAAAG

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**FIGURE 76**

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF  
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW  
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA  
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100.

FIGURE 77

**FIGURE 78**

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA  
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAAACGAGGCGGGTGGTG  
 CCTGCCCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT  
 TCTGTGCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCTT  
 CCTCCCCGCTCGTCCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA  
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC  
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGAC  
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA  
 TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCC  
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACTACTACATCCAGTGGCT  
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA  
 TCTTCCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG  
 GGTGTCTTGGGCCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT  
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT  
 ATGACTTTTGGGAGTACTATCTCCCCTACCTCTACTCATGCATCTCCTTCCCTTGGGGTTCTG  
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT  
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG  
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTG  
 CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGGCGGAAGGC  
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGCTGACGG  
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG  
 CCCCAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG  
 TGCCGTCAATCAGGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTATA  
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATT  
 GGGAACTGTGTCTGTCTCCTGGTCTAAGCTCAGCACTTCCTGTCTTCTCTCGAACCTGGG  
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA  
 TTGTGTTCTCTACAACGCAGCCTTTGCAGGCCTCACCACACTCTGTCTGGTGAAGACCTTC  
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCTTTGGGCTGGACAGACTGCCGCTGCCCGT  
 CTCCGGTTTCCCCCAGGCATCTAGGAAGACCCAGCACCAGTGAACCTCCAGCTGGGGGTGGGA  
 AGGAAAAAACTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGG  
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATT  
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAACCTGTGGCCT  
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAAATCTGTTTACACATCA  
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT  
 AGGGTGGGGTAGGGGAGGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC  
 CTTGCCTCTGGCCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTG  
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCCAGGGA  
 AAAAAA

**FIGURE 79**

MEAPDYEVLVSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK  
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGSLIHGLWNLVFLFPNLSL  
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMMLLLTLLVLGMVWVASAIVDKNKANRESL  
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRILLEDLEEQLYCSAFEE  
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT  
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFAGAVIQVVLIFYLMVSSVVGIFY  
SSPLFRSLRPRWHDAMTQIIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGIFY  
IVFLYNAAFAGLTTLCVLKFTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

**FIGURE 80**

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC  
GCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC  
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA  
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC  
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG



GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC  
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC  
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT  
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA  
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT  
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC  
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC  
GCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT  
CCATCATCAGCAATGAGGTGCTGCACTCCC

**FIGURE 82**

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTCTGACTGTAAGATCAAGTCCAAACCTGTTTT  
GGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCCATGCTGCTGT  
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCCATTT  
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGCAA  
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA  
TACTAAGAGAAACCCCAGACAATATCCTTGAGGTTT CAGGAATCTGGAGAGTACAGATGCCAG  
GCCCAGGGCTCCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC  
TCATGCTGCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCCTAGGCCTCTC  
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC  
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA  
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAAA  
AAA

**FIGURE 83**

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLLCKGFRFYSPQKTKWYHRYL  
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEMGFPHAAQANVELLGSSDLLT

**FIGURE 84**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGT  
GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG  
GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT  
GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG  
GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTTAAAAAGGCCTATAGGAACTAGCCCTGCA  
GCTTCATCCCCGACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG  
CTGCTTATGAGGTTCTGTCTAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA  
GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTT  
TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA  
TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT  
AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT  
GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT  
GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG  
AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG  
AGATTTACGGTTCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT  
TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT  
CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT  
ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA  
TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA  
CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG  
AATAAAATTGGACTTTGTTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT  
TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA  
TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGAATGACC  
AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGT  
TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA  
GTTGTTAGCAATTTCAATCAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG  
TTATTTT

**FIGURE 85**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQ  
 AQEKFQDLGAAYEVLSDSEKQYDQTYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGT PRQQ  
 DRNIPRGSDIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ  
 MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGM EY PFIGEGEPHVDGEPGDLRFRIKVVKH  
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD  
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

**FIGURE 86**

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA  
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT  
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG  
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAAAAGG  
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCTGATGATCCACAAGCCCAG  
GAGAAATTCCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA  
GTACGATAATTATGGTGAAGAAGGATTAAAAGATGGTNATCAGAGCTCCCATGGAGACATTT  
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA  
AATATTCCAAGAG

**FIGURE 87**

GGCACGAGGCGGCGGGGAGTCGCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT  
CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA  
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**  
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC  
TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC  
TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC  
TGGACGATGTGCTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC  
GAAGATGCCTCGGGTCTCATGTCCCCTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC  
AGAGAAGCTTGTTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA  
GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG  
TACCCTCCGTTGGACCCCCAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGTCAG  
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC  
AGTCTCTGTCGGCTGCTGAGGAGCATTGTGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG  
CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTT**TAG**TGCCT  
ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT  
CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTAGCTGTGTGTGCATAG  
TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGT  
GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA  
CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTCCTCAAGAAAATTGAGCCACCGTCT  
AAGAAATCAAGAGGTTTACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAATG  
TGTGGCAATTCTGATCTGCATTTTCAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC  
TTCTTTTGGCAAGACTTGTAATCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT  
GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGAGGTTTGGGTTTGAAGCTGAGGAACT  
ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG  
GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAAAAAA

FIGURE 88

METVVIIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSESEL  
ELDDVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSAS  
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI  
DQSLSAAEHLEVLREAALASEPDKGLPGPEGFLQEQSAI



**FIGURE 89**

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCC  
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA  
TTTGGAGTGTTTTTCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT  
TGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTGAGAT  
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTC  
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTTCAG  
GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT  
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACA  
AGTGAATTTGAAGACTCATTTAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA  
GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAAACGTATAG  
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA  
ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA  
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA  
CTGTGGTGCCTGTTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT  
TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA  
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAACCAAGGAAACCCCAATTTTG  
ATGTATGGATTACTTTTTTTTTGNGCNCAGGGCC

**FIGURE 90**

MISLTDTQKIGMGLTGFGVFLLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK  
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLLNLPGI  
RSFVDKVGESNNMV

**Important features:**

**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

**N-myristoylation sites.**

amino acids 11-16, 51-56 and 116-121

**Aminoacyl-transfer RNA synthetases class-II protein.**

amino acids 49-59

**FIGURE 91**

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC  
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA  
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTTCTGTTCTTTGGA  
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT  
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG  
CTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG  
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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**FIGURE 92**

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA  
GGCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGA  
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC  
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC  
ATCAACACCATTTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA  
GATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT  
CGGGCACGGAATGCACCATCTTCACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAT  
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA  
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA  
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT  
CGAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTTCCT  
GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC  
GGGCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC  
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTCAGAAA  
TAATGAAAATCCAACACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATG  
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC  
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCGAGA  
GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCCTCGTGAACCTGGCTGTTTTGGGCCTCGC  
TGGTGCTCTACCTTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG  
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT  
GACGGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACTG  
GACTCAGGGAGGTGTCACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT  
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCTGCTGGGCACGGCGGAAGTCACGA  
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT  
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC  
TGTGTGGTGAGTGTGAACCTTTGTTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG  
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCCTTTCATCCTTTGGTGCTGAGTTTTCTGT  
AACCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC  
CAAGAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

MDLAGLLKSQFLCHLVFCYVFIAASGLIINTIQFLTLLLWPINKQLFRKINCRLSYCISSQLV  
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNKFEIDFLCGWSLSERFGLLGSKVLAKK  
ELAYVPIIGMMWYFTEMVFCSRKWEQDRKTVATSLQHRLRDYPEKYFFLIHCEGTRFTEKKHE  
ISMQVARAKGLPRLKHLLPRTKGFAITVRS LRNVVSAVYDCTLNFRNNENPTLLGVLNGKK  
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTTFETPMVPPRRPWTLVN  
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS  
KQKLND

**FIGURE 94**

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG  
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA  
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA  
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTCTAGCTTTTATAATTCTTCAG  
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT  
 TGGTACAAATCCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA  
 AAACCTTGCAGGAGCATTTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAA  
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT  
 TTTTACAGGGTACCTTTAGTGTTGCCAATCTGGGCATGTCTGAACAACTGGGTTATAAAAC  
 TGTATCAGGTTCCCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT  
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA  
 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACT  
 AGTAAAGGATGTAAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGG  
 CAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGAACATTTTTCTTTGTCAGGCATTA  
 CGGACCTTTTTTCCAAATTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA  
 TGTTTCTAAAAGTAGCTGTAACACCAACCACATCTCGATGTAGTAGACAATCTGACCTTAA  
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT  
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA  
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC  
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA  
 TTTT**TGA**TCCTTTTAACTTACAAGGAGATTTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT  
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTAC  
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTTCAAAC  
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCT  
 TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA  
 TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC  
 TGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAAATGGAAAAGCAAGAATAGCCTTAT  
 TTTCAAATATGGAAAGAAATTTATATGAAAATTTATCTGAGTCATTAAAATTCTCCTTAAG  
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA  
 ATAAATTTGCAAAACATCATCTAAAATTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 95**

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGGEVKGEAKNSITDSQMDDVEVVYTIDIQ  
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH  
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC  
MSTGFSRAVQTHSSKFFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN  
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS  
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDDRWQFKRSRLLDLTQDKRSKA  
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTE

GGCACAGCCGCGCGCGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGC  
CCAAGCAGCGCGCAGCGAACGCCCGCCGCCGCCACACCCTCTGCGGTCCCCGCGGCGCCTGCCACCCTTCCCT  
CCTTCCCCGCGTCCCCGCCCTGCCCGCCAGTCAGCTTGCCGGGTTGCGTGCCCCGCGAAACCCCGAGGTCAACA  
GCCC GCGCCTCTGCTTCCCTGGGCCGCGCGCCGCTCCACGCCCTCCTTCTCCCCCTGGCCCCGGCGCCTGGCACC  
GGGGACCGTTGCCTGACGCGAGGGCCAGCTACTCTTTTCCGCCCCGCGTCTCCTCCGCTGCTCGCCTGCTTCCAC  
CAACTCCAACTCCTTCTCCTCCCTCAGCTCCACTAGTCCCCAGTCCGCGAGCCCTCGGCCCGCTGCCGTAG  
CGCCGCTTCCCGTCCGTTCCCAAAGGTGGGAACGCGTCCGCCCGGCCCGCACC**ATGGC**ACGGTTCCGGCTTGCC  
CGCGCTTCTCTGCACCCTGGCAGTGCTCAGCGCCGCGTCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG  
AAGTGCGACGTCTTTACGTGTCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT  
TTGAAGATCTGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGA  
TGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTCAAGTTACAAGAAGTTG  
ATGAATTTCTCAAAGAACTACTTGAAAATCGAGAAAGTCCCTGAATGATGTTTGTGAAGCATATGGCCAT  
TTATACATGCAAAAATCTGAGCTATTTAAAGATCTTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT  
GAACCTGGAAGAAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCCTGGTGAACCTCCAGT  
ACCACCTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT  
CGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTTCGCTCAAGGCTTAGCGGTTGCGGG  
AGATGTCGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT  
GCTCCCACTGCCGGGTCTCTGACTGTGAAGCCATGTTACAACACTGCTCAACCATCATGAGAGGCTGTTTG  
GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA  
GGGTCTTTCAACATTTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG  
ATAATAGTGTTCAAGTGTCTCAGAAGGTTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATT  
TCTCGTTCCATCTCTGAAAGTGCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCAACCCACAGC  
AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAAACTGAAACAGGGCCAAGAAATTTGTCCT  
CCCTTCCGAGCAACGTTTGCACGATGAGAGGATGGCTCGAGGAACCGCAATGAGGATGACTGTTGAAATGGG  
AAGGCAAAAGCAGGTACTGTTTGCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCA  
GGTTGACACCAGCAAACAGACATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA  
AGAATGCATACAATGGGAACGACGTGGACTTCTTTGATATCAGTCATGAAAGTAGTGGAGAAGGAAGTGGAAGT  
GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAAATGA  
GAAAGCCGACAGTGCTGGTGTCCTGGGGCAGAGCCTACCTCCTGACTGTCTTCTGCATCTTGTCTCTG  
TTATGCAGAGAGAGTGGAGT**TAAT**ACTTCAAACCTGAGAAAAAGTGTTTCATCAAAAAGTTAAAGGCCACCAAGTT  
ATCACTTTTCTACCATCCAGTACTTTGCTTTTTTAAATGAATGGACAACAATGTACAGTTTTTTACTATGTGGC  
CACTGGTTTTAAGAAGTGCTGACTTTTGTCTTCTCATTGATTTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGT  
TCCTGCTCCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGA  
TTTTATCACTCTATTATTTGTTTGTATGTTTTTCTCATTGCTTTGGGTTTTTTTTTCCAACCTGTGATCT  
CGCCTTGTTTTCTACAAGCAAAACAGGGTCCCTCTTTGGCCTGAACATGTACGTATTTCTGAAATATTAATA  
GCTGTACAGAGAGTGGAGT**TAAT**ACTTCAAACCTGAGAAAAAGTGTTTCATCAAAAAGTTAAAGGCCACCAAGTT



**FIGURE 97**

MARFGLPALCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ  
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKS LNDMF  
VKTYGHLYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEY  
LECVSKYTEQLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL  
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES  
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRSESASFARFRPHHPEE  
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLEF  
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGE  
GSGSGCEYQOCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**FIGURE 98**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT  
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA  
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC  
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC  
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA  
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC  
AGTGCCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA  
AAGCCAAACAAGCATTCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT  
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA  
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC  
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTTGCTCTC  
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT  
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCAATTAACCTTAAATGC  
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTTAAATGTCAAAAAAAAAAAAAAAAAA

**FIGURE 99**

MKVLISSLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR  
 KFMTVSGLPKKQCPDHFKGNVKTRHQRRHRKPNKHSRACQQLKQCQLRSFALPL

| Climatic Data |                  |
|---------------|------------------|
| Year          | Temperature (°C) |
| 1990          | 15.2             |
| 1991          | 14.8             |
| 1992          | 15.5             |
| 1993          | 16.1             |
| 1994          | 15.8             |
| 1995          | 16.3             |
| 1996          | 16.7             |
| 1997          | 17.1             |
| 1998          | 17.5             |
| 1999          | 17.9             |
| 2000          | 18.3             |
| 2001          | 18.7             |
| 2002          | 19.1             |
| 2003          | 19.5             |
| 2004          | 19.9             |
| 2005          | 20.3             |
| 2006          | 20.7             |
| 2007          | 21.1             |
| 2008          | 21.5             |
| 2009          | 21.9             |
| 2010          | 22.3             |
| 2011          | 22.7             |
| 2012          | 23.1             |
| 2013          | 23.5             |
| 2014          | 23.9             |
| 2015          | 24.3             |
| 2016          | 24.7             |
| 2017          | 25.1             |
| 2018          | 25.5             |
| 2019          | 25.9             |
| 2020          | 26.3             |
| 2021          | 26.7             |
| 2022          | 27.1             |
| 2023          | 27.5             |
| 2024          | 27.9             |
| 2025          | 28.3             |
| 2026          | 28.7             |
| 2027          | 29.1             |
| 2028          | 29.5             |
| 2029          | 29.9             |
| 2030          | 30.3             |
| 2031          | 30.7             |
| 2032          | 31.1             |
| 2033          | 31.5             |
| 2034          | 31.9             |
| 2035          | 32.3             |
| 2036          | 32.7             |
| 2037          | 33.1             |
| 2038          | 33.5             |
| 2039          | 33.9             |
| 2040          | 34.3             |
| 2041          | 34.7             |
| 2042          | 35.1             |
| 2043          | 35.5             |
| 2044          | 35.9             |
| 2045          | 36.3             |
| 2046          | 36.7             |
| 2047          | 37.1             |
| 2048          | 37.5             |
| 2049          | 37.9             |
| 2050          | 38.3             |
| 2051          | 38.7             |
| 2052          | 39.1             |
| 2053          | 39.5             |
| 2054          | 39.9             |
| 2055          | 40.3             |
| 2056          | 40.7             |
| 2057          | 41.1             |
| 2058          | 41.5             |
| 2059          | 41.9             |
| 2060          | 42.3             |
| 2061          | 42.7             |
| 2062          | 43.1             |
| 2063          | 43.5             |
| 2064          | 43.9             |
| 2065          | 44.3             |
| 2066          | 44.7             |
| 2067          | 45.1             |
| 2068          | 45.5             |
| 2069          | 45.9             |
| 2070          | 46.3             |
| 2071          | 46.7             |
| 2072          | 47.1             |
| 2073          | 47.5             |
| 2074          | 47.9             |
| 2075          | 48.3             |
| 2076          | 48.7             |
| 2077          | 49.1             |
| 2078          | 49.5             |
| 2079          | 49.9             |
| 2080          | 50.3             |
| 2081          | 50.7             |
| 2082          | 51.1             |
| 2083          | 51.5             |
| 2084          | 51.9             |
| 2085          | 52.3             |
| 2086          | 52.7             |
| 2087          | 53.1             |
| 2088          | 53.5             |
| 2089          | 53.9             |
| 2090          | 54.3             |
| 2091          | 54.7             |
| 2092          | 55.1             |
| 2093          | 55.5             |
| 2094          | 55.9             |
| 2095          | 56.3             |
| 2096          | 56.7             |
| 2097          | 57.1             |
| 2098          | 57.5             |
| 2099          | 57.9             |
| 2100          | 58.3             |

**FIGURE 100**

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT  
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA  
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA  
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA  
AACATTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA  
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC  
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC  
CTGACTGCATTTTTGCTTTTAGAAAAGTTAGAATAAAATATGGCGCTTTGGGATCACATAGTTG  
ATGGAGAGGAAA

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**FIGURE 101**

MAVLVLRLTVVLGLLVLFITCYADDKPDKPDDKPDDSGKDPKPDFPKFLSLLGTEIIENAVE  
FILRSMRSTGFMEFDDNEGKHSSK

0994650  
T094650

**FIGURE 102**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT  
CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTAC  
CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAAGCTACTTCC  
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG  
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG  
CTGCGGAACCGGAGCCAACTTTAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC  
CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT  
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT  
GGTGGTCTGCACTCTGGTGCTGTGCTCTGTGCAGAGCCCCAAGGAAGGTCTGCAGGAGGTCC  
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA  
AGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCCACCTGGAAACACATTGGGGATGGCTG  
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCCAGTTCTCCGAAATCCAAATGG  
AAGCAGACCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC  
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA  
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCT**TAG**CAGAATGAGAGAAGACATT  
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC  
CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC  
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC  
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT  
CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT  
CTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT  
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA  
AACCACG

| Parameter                | Unit  | Value |
|--------------------------|-------|-------|
| Temperature              | °C    | 25.0  |
| Pressure                 | atm   | 1.0   |
| Flow rate                | L/min | 1.0   |
| Sample concentration     | mg/mL | 1.0   |
| Sample volume            | μL    | 1.0   |
| Injection volume         | μL    | 1.0   |
| Column length            | m     | 1.0   |
| Column diameter          | mm    | 1.0   |
| Column packing           | μm    | 1.0   |
| Mobile phase             |       | 1.0   |
| Detection wavelength     | nm    | 1.0   |
| Scan rate                | °/min | 1.0   |
| Resolution               | nm    | 1.0   |
| Signal-to-noise ratio    |       | 1.0   |
| Peak area                | μg    | 1.0   |
| Peak height              | μg    | 1.0   |
| Retention time           | min   | 1.0   |
| Standard deviation       | μg    | 1.0   |
| Correlation coefficient  |       | 1.0   |
| Regression equation      |       | 1.0   |
| Intercept                | μg    | 1.0   |
| Slope                    | μg    | 1.0   |
| Y-intercept              | μg    | 1.0   |
| X-intercept              | μg    | 1.0   |
| Mean square error        | μg    | 1.0   |
| Adjusted R-squared       |       | 1.0   |
| F-statistic              |       | 1.0   |
| P-value                  |       | 1.0   |
| Confidence interval      | μg    | 1.0   |
| Limit of detection       | μg    | 1.0   |
| Limit of quantification  | μg    | 1.0   |
| Recovery                 | %     | 1.0   |
| Stability                | %     | 1.0   |
| Precision                | %     | 1.0   |
| Accuracy                 | %     | 1.0   |
| Linearity                | %     | 1.0   |
| Robustness               | %     | 1.0   |
| Specificity              | %     | 1.0   |
| Sensitivity              | %     | 1.0   |
| Reliability              | %     | 1.0   |
| Validity                 | %     | 1.0   |
| Feasibility              | %     | 1.0   |
| Practicality             | %     | 1.0   |
| Cost-effectiveness       | %     | 1.0   |
| Time efficiency          | %     | 1.0   |
| Space efficiency         | %     | 1.0   |
| Energy efficiency        | %     | 1.0   |
| Material efficiency      | %     | 1.0   |
| Human efficiency         | %     | 1.0   |
| Environmental efficiency | %     | 1.0   |
| Social efficiency        | %     | 1.0   |
| Economic efficiency      | %     | 1.0   |
| Overall efficiency       | %     | 1.0   |

| Parameter               | Unit  | Value |
|-------------------------|-------|-------|
| Temperature             | °C    | 25.0  |
| Pressure                | atm   | 1.0   |
| Flow rate               | L/min | 1.0   |
| Sample concentration    | mg/mL | 1.0   |
| Sample volume           | μL    | 1.0   |
| Injection volume        | μL    | 1.0   |
| Column length           | m     | 1.0   |
| Column diameter         | mm    | 1.0   |
| Column packing          | μm    | 1.0   |
| Mobile phase            |       | 1.0   |
| Detection wavelength    | nm    | 1.0   |
| Scan rate               | °/min | 1.0   |
| Resolution              | nm    | 1.0   |
| Signal-to-noise ratio   |       | 1.0   |
| Peak area               | μg    | 1.0   |
| Peak height             | μg    | 1.0   |
| Retention time          | min   | 1.0   |
| Standard deviation      | μg    | 1.0   |
| Correlation coefficient |       | 1.0   |
| Regression equation     |       | 1.0   |
| Intercept               | μg    | 1.0   |
| Slope                   | μg    | 1.0   |
| Y-intercept             | μg    | 1.0   |
| X-intercept             | μg    | 1.0   |
| Mean square error       | μg    | 1.0   |
| Adjusted R-squared      |       | 1.0   |
| F-statistic             |       | 1.0   |
| P-value                 |       | 1.0   |
| Confidence interval     | μg    | 1.0   |
| Limit of detection      | μg    | 1.0   |
| Limit of quantification | μg    | 1.0   |
| Recovery                | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
| Linearity               | %     | 1.0   |
| Robustness              | %     | 1.0   |
| Specificity             | %     | 1.0   |
| Sensitivity             | %     | 1.0   |
| Reliability             | %     | 1.0   |
| Reproducibility         | %     | 1.0   |
| Stability               | %     | 1.0   |
| Precision               | %     | 1.0   |
| Accuracy                | %     | 1.0   |
|                         |       |       |

**FIGURE 104**

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG  
CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA  
ACTAATATTTATATGACAGAAGAAAAAGATGTCAATCCGTAAAGTAAACATCATCATCTTGG  
TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG  
TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAAA  
TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG  
AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTACAGACAACACTCGCTCCAAT  
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAG  
TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCCTAAACTTTTGGAAGGAA  
AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC  
TTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA  
AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG  
AAGATTGTGATTACGCCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTAC  
ATTGGCTATCTTGACTATAAAAAGGAAAGAATTTCGTAAAGCTTTCCATGAAAGCCAGCACTTG  
CTCATTTAATCCTGGAGTTTTTGTGTCAAACCTGACGGAATGGAAACGACAGAATATAACTA  
ACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT  
GGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC  
TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA  
AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT  
ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCAACCTAATCCGAAG  
ATATACCGAGATCTCAAACATAAAGTGAAACAGAATTTGAACTGTAAGCAAGCATTTCTCAG  
GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA  
GCAAGCCATGGAAAAAGATGTGTAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC  
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTT  
ACTACAATGCTGAATGACTGGAAAGAAGAAGTATGATATGGCTAGTTCAGCTAGCTGGTACAGA  
TAATTCAAACTGCTGTTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAAATAAACTT  
ACATTTTTC



MSFRKVNII I I L V L A V A L F L L V L H H N F L S L S S L L R N E V T D S G I V G P Q P I D F V P N A L R H A V D G R  
Q E E I P V V I A A S E D R L G G A I A A I N S I Q H N T R S N V I F Y I V T L N N T A D H L R S W L N S D S L K S I R Y K  
I V N F D P K L L E G K V K E D P D Q G E S M K P L T F A R F Y L P I L V P S A K K A I Y M D D D V I V Q G D I L A L Y N T  
A L K P G H A A A F S E D C D S A S T K V V I R G A G N Q Y N Y I G Y L D Y K K E R I R K L S M K A S T C S F N P G V F V A  
N L T E W K R Q N I T N Q L E K W M K L N V E E G L Y S R T L A G S I T T P P L L I V F Y Q Q H S T I D P M W N V R H L G S  
S A G K R Y S P Q F V K A A K L L H W N G H L K P W G R T A S Y T D V W E K W Y I P D P T G K F N L I R R Y T E I S N I K

TGGTTTTTTGCCCCATAAATTC CCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT  
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT  
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT  
TGCAGCTATAAACAGCATT CAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC  
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCTGAAAAGCATCAGA  
TACAAAATTGTCAATTTTGACCCTAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA  
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG  
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC  
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC  
TAAAGTTGTCATCCGTGGAGCAGGAAA

**FIGURE 107**

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG  
GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGAGGGAACGCGGGCGGCCAGACAACGGGC  
TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGGCGCGGGCTGCA  
TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT  
TGTCGGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT  
TTCCGATCACTTCAAAGTGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT  
CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC  
CATAACTTCCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTCAGGAATTGTAG  
GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA  
GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA  
ACAGCATTCAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA  
GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG  
TCAATTTTGACCCTAACTTTTGGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC  
ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCCAGCGCAAAGAAGG  
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA  
CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT  
CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA  
TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC  
CTGACGGAATGGAAACGACAGAATATACTAACCAACTGGAAAAATGGATGAAACTCAATGT  
AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACACCTCCTCTGCTTATCG  
TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT  
GCTGGAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA  
TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA  
GACCCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA  
CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGGAAG  
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAG  
GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT  
ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA  
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT  
GTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTTCAATAGGTAAAAA

**FIGURE 108**

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT  
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG  
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC  
GCCATCGTCTGCAACGGTCTCGTGCGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG  
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC  
TGGCCCCTGTCCTGAGAAGGCCCCACCACCCAGAAAGCCCAGCCATGAAGGCAGCTACCTGC  
TGCAGCCCCTGAAGGGCCCCTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG  
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT  
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC  
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT  
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC  
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG  
GCTGGGGCCCCCTCCCCTGGTCTCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA  
AAAAAAAAAAAAAAAAAAAA

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**FIGURE 109**

MGAAISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH  
PRSPAMKAATCCSPEGPWPSLEPRT

[illegible]

**FIGURE 110**

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA  
GTTCCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA  
CTCCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAA  
TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC  
ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTCAATTGGTTAT  
TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC  
TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTA  
TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT  
GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC  
AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCCTCTGGGTGGCTGTGCTGCTG  
AGCCTGGGAACTGCAGGAGCTGCCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCCCT  
TTCGGGCATTTCGGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA  
TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT  
AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA  
AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCA  
TGTAATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA  
TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA  
TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAGATGCATTCAAAATCT  
TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTA  
GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG  
GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGCCTACTTAGTAGCCC  
ATAGTTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCATTTTCTGTGTTTTGCTGTTGAT  
CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT  
CGTAAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA  
ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCT  
GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT  
AGTGAATTTTTTTTTTAAAAGACCTAATAAACCCCTATTCTTCTCCTCAAAA

**FIGURE 111**

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYYDYTNDL  
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ  
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI  
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM  
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL  
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH  
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN  
EEGTELQAIVR

GTTTCGATTAGCTCCTCTGTGAGAAGAAGAGAAAAGGTTCTTGACCTCTCCCTGTTTCTTCTCTT  
 AGAATAATTTGTATGGGATTTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTG  
 TGTGGTGAAAATTTTTTGAIAAAAAAAAAATTGCCTTCTTCAAACAAGGGTGTCAATTCTGATATT  
**TATG**AGGACTGTTGTTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCCCTTGTTTTGCTGG  
 TGA CTGGAGTACATTCAAACAAAGAAACGGCAAAGAAGATTAAGGCCAAGTTCTACTGTG  
 CCTCAGATCAACTGCGATGTCAAAGCCGGAAGATCATCGATCCTGAGTTTCATTGTGAAATG  
 TCCAGACAGGATGCCAAGACCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACT  
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAGGAGGGAAAAATACTTT  
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTT  
 ATCCCTACCACGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAGAGGTTGTA  
 CCTACCCATCAGCTCTTACATACTCATCATCGAAAGTCCAGCTGCCCAAGCAGGTGAGACC  
 ACAAAGCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA  
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCACCACCTTGCCAAGGCCATCCCCTTCTG  
 CTGCTTCTACCACCAGCATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT  
 CTCTGGTCCACTGCCACATACACAAGCAGCAAAACAGGCCAGAGCTGATCCAGGTATCCA  
 AAGGCAAGATCCTTACGAGAGCTGCCTTCCGAAACCTGTTGGAGCGGATGTCAGCCTGGGAC  
 TTGTTCCAAAAAAGAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC  
 TGCAAAATTGACTTGTCTGTTTTTAATTGATGGGAGCACCAGCATTGGCAAACGGCGATTCCG  
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGCCCGTCCAC  
 TGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACACACAG  
 AATTCTCGATCTGAGAGACGCCATAGAGAAAATTACTCAGAGAGGAGCACTTCTAATGT  
 AGGTGCGGCCATCTCCTTTGTGACCAAGAACTTCTTTTCAAAGCCAATGAAACAGAAGCG  
 GGGCTCCCAATGTGGTGGTGGTGTGATGGTGGATGGCTGGCCACGGACAAAGTGGAGGAGGCT  
 TCAAGACTTGCGAGAGAGTCAAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGA  
 AAATGAGAAGCAGTATGTGGTGAGGCCAACTTTGCAAAACAGGCCGTGTCAGACAACAAG  
 GCTTCTACTCGCTCCACGTGCGAGAGCTGGTTTGGCCTCCACAAGACCCTGCAGCCTCTGGTG  
 AAGCGGGTCTGCGACACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAACCTCGGCTGACAT  
 TGGCTTCGTGATCGACGGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCACCGTCTCCAGT  
 TTGTGACCAACCTCACCAAGAGTTTGAGATTTCCGACACGGACAGCGCATCGGGGCCGTG  
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTGCACAAGTACAGCAGCAAGCCTGACAT  
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCAGCACGGGGGCTGCCATCA  
 ACTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAAGCCCAACAAGAGGAAGTTAATGATCCTC  
 ATCACCGACGGGAGGTCTACGACGACGTCCGGATCCCAGCCATGGCTGCCCATCTGAAGGG  
 AGTGATCACCTATGCGATAGGCCTTGCTGGCTGGCTGCCAAGAGGAGCTAGAAGTCAATTGCCA  
 CTCACCCCGCAGAGACCACCTCTTCTTTGTGGACGAGTTTGACAACCTCCATCAGTATGTC  
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTACAGAG  
 CAGGCAGAGCACCAGCAAGTGCTGCTTTACTAACTGACGTGTTGGACCACCCACCGCTTAA  
 TGGGGCACGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAACAAATGTCTTGTATTAT  
 TTCTTTGCCATCATGCTTTTTTCATATTCCAAACTTGGAGTTACAAGATGATCACAACAGT  
 ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGACAATT  
 GTTTTCAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT  
 GTGAGATTTTTTAAGTTGTTATTTCTGATTTGAACTCTGTAACCTCAGCAAGTTTCATTTTT  
 GTCATGACAAATGTAGGAATGCTGAATTAATGTTTAGAAGGATGAAAAATAAAAAAAAAA  
 AA  
 AAAG



**FIGURE 113**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC  
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL  
SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ  
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSQNRPRADPGIQ  
RQDPGGAFFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR  
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHNTSRDLKTAIEKITQRGGLSNV  
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE  
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTQLPLVKRVCDTDRLACSKTCLNSADI  
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISD TDTRIGAVQYTYEQRLEFGFDKYSSKPD  
LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG  
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRI IQNICTEFNSQPRN

**FIGURE 114**

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCT**A**  
**TG**CCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT  
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCCCTACAGTTTTTCTCTGACTCTAAT  
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG  
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT  
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA  
 GGCTGGATGGCCCTGTTCCGGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCCGAAAACCTCC  
 TCCCAGCCTTTCAGACCCCCCTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG  
 AACCCAGGAGAGACCCCTGTCACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC  
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC  
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC  
 AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT  
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCCCTAGAGTATAACAAAG  
 CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAAGTGTACAAGGGGACT  
 GTGTCCATGCCAGTCTTCCAGTCCCTTGAGGCGCTACTGGCCTGGTCTTCAGAGCCTCATTGG  
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG  
 GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGGCTACCCA  
 CTTCCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT  
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGCGGAT  
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCCTG  
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG  
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGGTACA  
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG  
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC  
 GAAATTTTCAAAAAACACTGTTAGTTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC  
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA  
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT  
 AGACTCCTCA**TAA**CCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA  
 AATTGCTTTTGGCTATCATAAAA

**FIGURE 115**

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE  
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRRMAEEAARKL  
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM  
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK  
AIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG  
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG  
FATIKDLRDHKL DNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY  
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT  
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

Figure 1 consists of 15 small plots arranged in a grid. Each plot shows the relationship between a specific variable and the probability of a 'Yes' response. The variables are listed on the left side of each plot. The plots are arranged in a grid with 3 rows and 5 columns. The first 10 plots show the relationship between 'Yes' probability and 'No' probability for different variables. The last 5 plots show the relationship between 'Yes' probability and 'No' probability for different variables. The variables are: (1) 'Yes' probability, (2) 'No' probability, (3) 'Yes' probability, (4) 'No' probability, (5) 'Yes' probability, (6) 'No' probability, (7) 'Yes' probability, (8) 'No' probability, (9) 'Yes' probability, (10) 'No' probability, (11) 'Yes' probability, (12) 'No' probability, (13) 'Yes' probability, (14) 'No' probability, (15) 'Yes' probability.

Figure 1 consists of 15 small plots arranged in a grid. Each plot shows the relationship between a specific variable and the probability of a 'Yes' response. The variables are listed on the left side of each plot. The plots are arranged in a grid with 3 rows and 5 columns. The first 10 plots show the relationship between 'Yes' probability and 'No' probability for different variables. The last 5 plots show the relationship between 'Yes' probability and 'No' probability for different variables. The variables are: (1) 'Yes' probability, (2) 'No' probability, (3) 'Yes' probability, (4) 'No' probability, (5) 'Yes' probability, (6) 'No' probability, (7) 'Yes' probability, (8) 'No' probability, (9) 'Yes' probability, (10) 'No' probability, (11) 'Yes' probability, (12) 'No' probability, (13) 'Yes' probability, (14) 'No' probability, (15) 'Yes' probability.

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## **FIGURE 117**

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSW  
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPLVLALFAFVGFMILIV  
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation sites.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins homology.**

amino acids 92-119

#### **Integrins alpha chain protein homology.**

amino acids 232-262

**FIGURE 118**

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC  
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

**FIGURE 119**

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCC**ATG**GTGGCGGCGACGGTGGCAGCGGCGTG  
GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG  
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG  
AATGTGGCCAGCGAGTGCGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG  
AGACCTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG  
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCGCACCTACAGTGTCTCATTCCCC  
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA  
GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG  
TGGTAGGGGCTTGGGACCCAACTGTGTCACTGGAGGAGGTGAGACCCAGATCACAGCGCTC  
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTA**TAA**CACCGCGTCTCCTCCTCCACCA  
CCTCATCCCGCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG  
AGACCCACTGACTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA  
AAATTCTAGTATTTTGAATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG  
AGCTCTTGACCAGTGAATCACCGAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAA  
TAGAAGTATATCAAGCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC  
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC  
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAAT  
AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT  
GTTATTTCTCCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA  
AACAATACCTCACGATATAAAATAAAAATGAAAGTATCCTCCTCAAAA

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**FIGURE 120**

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVVNVASECGFTDQ  
HYRALQQQLQRDLGPHHFNVLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG  
AHPAFKYLAQTSKGKEPTWNFWKYLVPDQKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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**FIGURE 121**

CGGACGCGTGGGCGGGCCGGGACGCGAGGCAAGCGAGGCC**ATGGCT**GTCTACGTCGGGATGCTGCGCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCCGGGCCGCCCTCTCTCGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCCAGAGAGGTGGATCGCATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTCAGGGGTGCACCAAAAAGCATCTTAACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCCTTGGTCTCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAAAGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGACTAACTCCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCCAGGCGGGCATCATTTCTGGTGCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCCTCAAGAAGGTGGGCTGCAAGGCCCTTGTTCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCTGTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCCAGATCTGACCACAGTCATCTCGGTGGATGCCCCCTTTGCCGGGGACCCTGCTCCTGGATGAAGTGGTGGCGGCTGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTTCTGTCTTGCCATGACCCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCCTCTCCACTACAACATTGTCAACAACCTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTGATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGAACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCAATTGCTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAACAGTCCCGTGACATTTCGCGCACTTCCCTGAGGACACTGTGAGCAGAAAGGCAGAAAGCGTGGGCAGAAATTATGCCTCACACGGAGGCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGGCTTCTGCAAGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAGCTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGACGATCGGATGGGGGAAGAGATTTGTGCCTGCATTTCGGCTGAAGGACGGGGAGGAGACCACGGTGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATCGTGTTTGTACAAACTACCCCTCACCATTTTCAGGAAAGATCCAGAAATTCAAACTTCGAGAGCAGATGGAACGACATCTAAATCTGT**TGA**ATAAAAGCAGCAGGCCTGTCCTGGCCGGTTGGCTTGACTCTCTCCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTCGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAACTAAGAGCTCCTGGATGGGTCGGGAACTCGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCCAGGCCCTCCCTCCTGTCCATCCCCCACATTCCCCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTTGAAAAAAAAAAAAAAAAA

**FIGURE 122**

MAVYVGMLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLSSREVDRMVSTPIGGLSYVQ  
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG  
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY  
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDEVVAAGSTRQHLDQLQYN  
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY  
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY  
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG  
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT  
MNEQGFCCKIVGRSKDMIIRGGENIYPAELEDDFFHTHPKVQEVQVVGVKDDRMGEEICACIRL  
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domains:**

amino acids 140-161, 213-229, 312-334

**Putative AMP-binding Domain Signature:**

amino acids 260-271

**N-myristoylation Sites:**

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,  
314-319, 318-323, 379-384, 380-385, 409-413

**N-glycosylation Site:**

amino acids 282-285

**FIGURE 123**

CAACTCCAACATTTTAGGAGAGCGCCTGAACTGCATGAGAAGACACCAGAGCAGTTGCGGA  
TGATCCTGCCCCAACCCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG  
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC  
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA  
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC  
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT  
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG  
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG  
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGAGCTGTGCATCCGAGGGTACTGCGT  
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT  
ATTGGACAGGAGATGTCGCCAC

**FIGURE 124**

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC  
AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG  
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC  
GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC  
AGTGCGGGGTTCGCGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC  
TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC  
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCAACGGCGTGAGTG  
CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCGTGAGCT  
GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA  
GCTAATGTGACTGTGTCCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA  
TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAC  
CTGACCTCCGCAACAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCT  
CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACCACTTCTACCTCGGCCCCAGTGAG  
ACCCACATCCACCACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAG  
AACACGAGGCCTCCCGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC  
CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG  
TGTGGCTCCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTCTACTGTT  
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT  
CATCACTTCCTGTTCCCACTGGACTGGGCTGGCCCAGCCCCTGTTTTTCCAACATTCCC  
CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGCGGCTTTGGGAAATAAAATACCGTTGTATAT  
ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC  
TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTG  
AGAGAGAGGATGCTAAGCTTCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG  
GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGG  
GAATCGGTTCCCCATATGTCTTCCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC  
CCAATTCGCCCTATAGTGAGTCGTA

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**FIGURE 125**

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT  
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFLQLQQCAQDRCAKLNLTSRAL  
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV  
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT  
VASTTSVTTSTTSAPVRPTSTTKMPAPTSQTPRQVEHEASRDEEPRLTGGAAGHQDRSNSG  
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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**FIGURE 126**

CGGGACTCGGCGGGTCCTCCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT  
TGGTGCTGGTCTTCCTCTGCAGCCTGCTGGCCCCATGGTCCTGGCCAGTGCAGCTGAAAAG  
GAGAAGGAAATGGACCCTTTTTCATTATGATTACCAGACCCTGAGGATTGGGGGACTGGTGTT  
CGCTGTGGTCCTCTTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTT  
TCAATCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCTCATCACCGCC  
AATGCAACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAA  
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAATGTGATGCT**TAAG**AAAACCGGCCACTTC  
AGCAACAGCCCTTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCTATCCCCTCTA  
ACACCATTCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCGGTCTT  
GCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTG  
GTCTTTGTGGCTACTTGTTTGTGGATGGTATTGTGTTTGTAGTGAAGTGTGGACTCGCTTT  
CCCAGGCAGGGGCTGAGCCACATGGCCATCTGCTCCTCCCTGCCCCCGTGGCCCTCCATCAC  
CTTCTGCTCCTAGGAGGCTGCTTGTTGCCCGAGACCAGCCCCCTCCCCTGATTTAGGGATGC  
GTAGGGTAAGAGCACGGGCAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGCAGCAC  
TTTGTGTCATATTCTTCATGGACTCCTTTCACTCCTTTAACAAAAACCTTGCTTCCTTATCCC  
ACCTGATCCCAGTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCC  
CAGCGTTGACGTCAGGCAGGCTATGCCCTTCCGTGGTTAATTTCTTCCCAGGGGCTTCCACG  
AGGAGTCCCCATCTGCCCCGCCCCCTTACAGAGCGCCGGGGATTCCAGGCCCAGGGCTTCT  
ACTCTGCCCCCTGGGGAATGTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG  
GACCCTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCCAGCTCATCCAG  
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCC  
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCCTTTGCTTCTCTGCCTACG  
TCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGTCGGTGGTCAGA  
GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAG  
GTTGAAGGTCATAACGAGAGTGGGAACCAACCCAGATCCCGCCCCCTCCTGTCTCTGTGTT  
CCCGCGGAAACCAACCAACCGTGCGCTGTGACCCATTGCTGTTCTCTGTATCGTGATCTAT  
CCTCAACAACAACAGAAAAAAGGAATAAAATATCCTTTGTTTCCT

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**FIGURE 127**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK  
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTevQPSGGSLWNLRRLLLEPLDANVDA

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**FIGURE 128**

AAACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT  
CCTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG  
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT  
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT  
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT  
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT  
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA



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**FIGURE 129**

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE  
FLNWHALFESIKRKLPFLNWDAFPKLGKGLRSATPDAQ

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**FIGURE 130**

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC  
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTC  
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC  
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTTAGAATACTGTTGACTTCT  
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA  
AATTTTTGTTATACTAGATGGCTTCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT  
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTCATC  
TTCATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT  
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCACAAATGTGATTGTTAATTTAA  
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT  
AAAAGTTTTGAGTATATTTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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**FIGURE 131**

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

Figure 1 consists of 12 sub-charts, labeled (a) through (l), arranged in a 6x2 grid. Each sub-chart displays the percentage of total protein for various protein types (A, B, C, D, E, F, G, H, I, J, K, L) across different conditions (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12). The y-axis for each chart represents the percentage, with scales ranging from 0 to 100. The x-axis for each chart lists the protein types. The data is presented as horizontal bars, with the length of the bar indicating the percentage. The charts show varying distributions of protein types across the fractions, with some fractions showing higher percentages of certain protein types than others.

**FIGURE 132**

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG  
GCTGCTGTTGTTTCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA  
AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC  
TGCAGCTGCTACCATGGTGT CATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG  
GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA  
GACTGTACCGGGAAAATGACTGCATGTTCCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT  
TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA  
GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC  
ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT  
CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG  
GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG  
ATCCTCTCATTTCTTCTGTCTCGGAAAAACCCAAAACCTTGTTGATGCAGAATACACCAAAAAC  
CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT  
GGATCACTGCAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA  
AACACCTCTTCCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC  
TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCA  
AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA  
GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG  
AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT  
TCCCAAATGTTGAAAACCTGAACCTATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCA  
ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA  
TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA  
AAGATTTAAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA  
CCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCATTTTCTTAAGACCAATC  
ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA  
TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTCGTCATTTGGAAGTAGTACAA  
CTCATTGCTGGAATTGTGAAATTATTTCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG  
AAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG  
TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTTACTCAG  
GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT  
TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

**FIGURE 133**

MEWWASSPLRLWLLLFLLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCSSQNCSCYHGVIE  
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD  
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL  
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT  
LGKPAAKDVHLVDHCKYKYLENFRGVAASFRFKHLFLCGSLVFHVGDEWLEFFYPQLKPWVH  
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY  
NVTRRKGYDQIIPKMLKTEL

**FIGURE 134**

CACCCCTCCATTTCTCGCCATGGGCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT  
TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT  
GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA  
CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC  
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCTTCAG  
AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCAGCTGGTGATGCGGTACTGGGAGCC  
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC  
TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT  
GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC  
TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG  
TGGAGCTGCTGACAGTGCTGTGGGTGGTGCCCTACCCTGGGCACGGACCGTCTCCTCCTTGCT  
TTCCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT  
CCGGGCCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT  
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCCTCTCCCACTGAATTCTAAATCCTTAAC  
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCCCTT  
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA  
CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC  
TTCCTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC  
CTGACCACTCCCCTGGCACTGTTACTTGCCTCTGCGCCTCAGGGGTCCCCCTTCTGCACCGCT  
GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA  
GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT  
GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC  
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

**FIGURE 135**

MAPALLLIPAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP  
LAWDLGLLLLLFVGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV  
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP  
RALRLFSHLRHPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR  
KLHLLSRPQDGEAE

**Signal sequence:**

amino acids 1-13

**Transmembrane domains:**

amino acids 58-76, 99-113, 141-159, 203-222

**N-myristoylation sites:**

amino acids 37-43, 42-48, 229-235

**FIGURE 136**

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA  
AGAAATTGCCAAACCATGTCTTTTTTTCTGTTTTTCAGAGTAGTTCAACAACAGATCTGAGTGT  
TTTAATTAAGCATGGAATACAGAAAACAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATT  
CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA  
TCACGTGGTGCTCTCCGACTACTCACCCCGAGTGTAAAGAACCTTCGGCTCGCGTGCTTCTG  
AGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCC  
CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT  
TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT  
ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT  
CTGGTCATTCTGGTGACCTCCCAACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC  
TTGGGGTGAAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG  
AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCTTAGAGGATGAACACCTTCTTTATGGT  
GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC  
ATTCAGGTGGGTAACTGAGTTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG  
TTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT  
TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATAT  
TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTATATATA  
TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAAACCCATCAAGTTT  
GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAAAGTGAACATTCATATTCAGAAGA  
CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG  
CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACC  
ACATGCCATTATTAACTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA  
GTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTTACACTG  
AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTC  
AGGCCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAA  
GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGG  
TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTTATTG  
AACAAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA  
TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT  
TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAAATTA  
CTTCAACTTTGTGTTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT  
CATTCTTTACATGCAAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC  
TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAAT  
ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA



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**FIGURE 137**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPiYRQD  
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK  
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTLKTIMAFRWVTEFCPNAKYVMKTD TDVFIN  
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYCSGLGYIMSRD  
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG  
FSSKEIITFWQVMLRNTTCHY

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"T.F. 63/65"

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT  
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA  
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA  
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAAATGGCTTTGCTGCAACC  
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT  
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC  
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA  
AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC  
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT  
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT  
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT  
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

**FIGURE 139**

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS  
IWDYGNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN  
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

**Signal Peptide:**

amino acids 1-20

**N-myristoylation Sites:**

amino acids 67-72, 118-123, 163-168

**Flavodoxin protein homology:**

amino acids 156-174

**FIGURE 140**

CATTTCTGAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA  
TTAACTTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCG  
CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTCTTATTGCTTACTGATTTTTT  
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA  
GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG  
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT  
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT  
CAGATTCCGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAAT  
CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC  
TGGAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTAAAAGCAAAGGGA  
TTGAATCCGGATGGAACCTCAGCCCTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC  
ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG  
TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAGAAAA  
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG  
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA  
GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT  
GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG  
TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG  
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT  
GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG  
CTGACTTTCTCTTCCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT  
ATGGACTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTTGATTTCTTGAAACCCTCTA  
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTTGCACATT  
AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT  
TGTGTATTGTTTATTGCTATAAGA ACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTT  
ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT  
ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAAATACAAAT  
CTTGTTTTTTTCTAAAAA AAAAAAAAAAAGT

**FIGURE 141**

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLLEFGTTEEEIQEICIETLRLY  
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK  
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN  
NRRSRSGTYSSRSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRSRSQ  
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHRR

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TGGGGATAAAGGAAAAATG<sup>1</sup>GTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA  
TTTTTTGAANNATATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT  
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT  
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTN<sup>2</sup>TTATTGCTTACTGATTTTTTTG  
AGTTAAGAGTTGTTATATGNTAGAAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAAGA  
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGA<sup>3</sup>ACTGGTTTGTTTACATGCA  
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT  
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA  
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAATCC  
AGGAAATNTGCATAGAAACACTTAGGC<sup>4</sup>TTTATACCAGAAAAAAGCCAAACTATGAATTACTG  
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT  
GAATCCGGATGGA<sup>5</sup>ACTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

**FIGURE 143**

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGTCA**ATGGC**  
GGTCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC  
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTTTGTTCGGATACAAGCACCCG  
TCTGAGGAGGAGCTTCGGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG  
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG  
AGACCTGCCCCCTCACGACCGTGATGCCCTGGTCCTGCGCTTCTTCCTGGAGTACCAGTGG  
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTCACAGAGGCCTACTACTACAT  
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT  
CCATCAAGATGTTCCCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC  
TCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG  
GGAGGAGACCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC  
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAGCTGGCTATCCGCGTG  
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCCAGGCCTGCGGCTGGC  
CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCCTCCTGC  
ACACCAGCTTCCTGTCTCCCCTGTTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC  
TTCCTGCACCAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA  
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC  
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC  
CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT  
GAGCTTGCAGTACCTGACGCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC  
TGGGAGGCTATTTCCTGGGGCCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC  
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG  
GGCCCTGGGTGGCCTGCTTACTCCCCTCTTCCTCCGTGGCGTCCTGGCCTACCTCATCTGGT  
GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA  
GGCTCC**TAG**CTGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA  
CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC  
GGCGTTCCCTTACACACAGTGCCCTGACCCGCGGCCCCCCTTGGACGCCGAGTTTCTGCCTCA  
GAACTGTCTCTCCTGGGCCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG  
TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC  
GATTTTTAA

**FIGURE 144**

MAVLGVQLVVTLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEEELRALAGKPRPRGRKE  
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY  
YMLGPAKETNIAVFWCLLTVTFSIKMFLT VTRLYFSAEEGGERSVCLTFAFLFLLLAMLVQV  
VREETLELGLEPGLASMTQNLEPLLKKQGWDWALPVAKLAI R VGLAVVGSVLGAFLT F PGLR  
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA  
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT  
VVSLQYLTPLILT LNCTLLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI  
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLAGS



**FIGURE 145**

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC  
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT  
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGGCCCTGGCGGGGAAGCCGAGGCC  
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC  
GAGATGCCCCGTTCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC  
TTCTTCCTGGAGTACCACTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT  
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT  
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTTCCTGACAGTGACACGGCTGTACTTCAGC  
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC  
CATGCTGGTGCAAGCG

GTTTCCTACATCCTCTCATCTGTAGAATCAGAGAGCATAATCTTCTTACGGGGCCGCGTATTATTAAACGTGGCTT  
 AATCTGAAAGGTTCTCAGTCAAATTTCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC  
 TTGGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGA**ATGA**AGG  
 CGCTTCTGTTGCTGGTCTTGCTTGGCTCAGTCTCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTTG  
 TATTCAGAACTCTGTAAAGGTGCCTCCCCTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAAGATGGCTG  
 TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA  
 TGACAGACGAGCCTGGCCTAGACAACCTCGCTACGTTCTCTCGGCAGGAGCAGGGCAGCAATCAGCCCA  
 GTGGACTCTGGCCGGGACCAACCGAACTAGGGCAGGCGCCTTTGAGAGATCCAATTATTAGAAGCAGATCATTTAA  
 AAAATAAATCGAGCTTTGAGTGTTCTTCGAAGGACAAAGAGCGGGAGTGCAATTGCCAACCATGCCGACCAGG  
 GCAGGGAAAAATTCTGAAAACACCACTGCCCTGAAGTCTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAA  
 ATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC  
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG  
 GAGACATCATTTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCAACAATACGCTGTGCGTCTCCTCGGG  
 CAGCCCTGCCAGGTGCTGTGGCTGAGTGTGATGCGTGAACAGAAGTTCCGCAGCAGGAACAATGGACAGGGCCC  
 GGATGCCATCAGACCCGAGATGACAGTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGA  
 TAAACTGGTGCGCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA  
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAGAAAG  
 TGCGGCTCATCTGATTACAGGCCAGTGAAAGACGTGTTACCTCGTGTGTCCCGCCAGGTTCCGCAGCGGAGCC  
 CTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT  
 CCCAAGCCCCCTCCATCCTACAATTACTTGTATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTTGAATCTCT  
 CGGCATGACCTCGCAGGGGAGCATCACATAGAGAATGGGATTTGCCATATCTATGTATCATAGTGTGAGCCG  
 GAGGAGTCATAAGCAGAGATGGAAGATAAAAAACAGGTGACATTTTGTGTAATGTGGATGGGGTCGAACTGACA  
 GAGGTGAGCCGGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT  
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCA  
 GTGACTGGTCCCCATCCTGGGTGATGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTA  
 CGAAGAAACACAGCTGGAAGTCTGGGCTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAACACAACCTTT  
 TTTTCATCAATCCATTGTTGAAGGAACCCAGCATACAATGATGGAAGATTAGATGTGGTGATATTCTTCTGTG  
 CTGTCAATGGTGAAGTAGACATCAGGAATGATACATGCTTGCTTGGCAAGACTGCTGAAAGAATTAAGGAAGA  
 ATTACTCTAACTATTGTTTCTTGGCCTGGCACTTTTTTTAT**TAGA**ATCAATGATGGGTGAGGAAAAACAGAAAAA  
 TCACAAATAGGCTAAGAAGTTGAAACACTATATTTATCTTGTGAGTTTTTATATTTAAAGAAAGAATACATTGT  
 AAAAATGTCAGGAAAAGTATGATCATTAATGAAAGCCAGTTACACCTCAGAAAATATGATTCAAAAAAATTA  
 AAACACTAGTTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTACAACATTGTTTATATTTTTTCTATTCAAT  
 AAAAGCCCTAAACAACTAAAAATGATTGATTTGTATACCCCACTGAATTCAAGCTGATTTAAATTTAAATTT  
 GGTATATGCTGAAGTCTGCAAGGGTACATTATGGCCATTTTAATTTACAGCTAAAAATTTTTTAAATTGCA  
 TTGCTGAGAAACGTTGCTTTCATCAAAACAAGAATAAATTTTTTCAAGGTTAA

**FIGURE 147**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT  
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRS  
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP  
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL  
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGV  
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQRS  
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE  
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV  
KEYEPQEDCSSPAALDSNHNMAPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV  
GGYEEYNGNKPF FIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI  
TLTIVSWPGTFL

**FIGURE 148**

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT  
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAA**ATG**GTGCTGACCATCT  
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC  
AATGTTCAAGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC  
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC  
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT  
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG  
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC  
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT  
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG  
TGCAGACATTCATGTT**TAG**GATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC  
TTGGTTTACACTCAAAAGTCAAATTAAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTC  
AGTCAGAAAATATAAATGCTGTATTTATA

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**FIGURE 149**

MKILVAFLVVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSST  
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMF SNKYTWVKYNPLE  
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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**FIGURE 150**

GGCACGAGCCAGGAACTAGGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC  
**ATG**GGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG  
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTCCCCAAAG  
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC  
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT  
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT  
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG  
CCAGTGTCTGAGCTGCGGGCCAATTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA  
GATGATCTGCCAGGCGTCCTCGGGCAGCCCACCTATCACCAACAGCCTGATCGGGAAGGATG  
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG  
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC  
CCTCACAGTGGTGCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA  
GCCCCATCCTTGCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG  
GGGTTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAAGCAGCAGCCATG**TAGA**ATGAACC  
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTTCTGTTTGGGA  
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 151**

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL  
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK  
PVSELNANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCHRQPANFSFLP  
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG  
GFRIGNGEVRGRKAAAM

### **Signal Peptide:**

amino acids 1-18

### **N-glycosylation Sites:**

amino acids 86-89, 132-135, 181-184

099766-11601

**FIGURE 152**

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG  
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT  
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA  
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAAA  
CTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT  
TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCCCTGC  
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT  
TTCGATGGGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC  
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT  
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC  
CTGGAGCCAAGTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCAC  
AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCA  
TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACG  
GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGT  
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCCTT  
TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC  
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC  
TCTTTTGTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT  
GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG  
AATTTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT  
TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA



**FIGURE 153**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF  
HYDCGNKTVTPVSPGLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR  
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS  
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 224-246

**N-glycosylation site.**

amino acids 68-72, 82-86

**N-myristoylation site.**

amino acids 200-206, 210-216

**Amidation site.**

amino acids 77-81

GGGAAAGCCATTTTCGAAAACCCATCTATACAAACTATATATTTTTCATTTCTGCTGCTAGCTG  
CCTTGGGCCTCACAAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAATGGAG  
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG  
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAATCATGAACTCTGGCTGTTGATCAAAA  
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC  
TCAACCTGGCCTCCCATAAACAGGACAGATTATTTCAGGTGATGGCAAAAATGGATTCTACAT  
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAAC  
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCTGTCGTACATGCTCAACAGC  
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT  
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGCAGCAAGGGACC  
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTTCCTGTAT  
CATCCTTTTCAATAAACTGTATTTCATTTTGAAAAAAAAAAAAAAAAAAAAA



GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**  
 CTCTTGTGGCAGGTAATCTGCAACCACACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA  
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC  
 AGAACTGCCCCTCCGTTTGTCTCGTGCAGTAACCAGTTCAGCAAGGTGGTGTGCACGCGCCGG  
 GGCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA  
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCAGT  
 TGGGCAGGAATCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAAC  
 ACCCTGGAGCTGTTTCGACAACCTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTC  
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCTCTTACGCCTTCA  
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT  
 GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA  
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACT  
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCATG  
 AACTCACAGGTGAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACCTTGTTGGAAC  
 CAACTTGCCCAACAATAACCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC  
 TGGTGGAGTTGCATCTACACCACAACCCCTTGGAACCTGTGATTGTGACATTCTGTGGCTAGCC  
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTCCCAT  
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCT  
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTTCGGATGGCAGAACCTTAAGTGT  
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC  
 CTCCCGCCACCCAAGGATCTCTGTCCTCAACGACGGCACCTTGAACCTTTTCCCACGTGCTGC  
 TTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG  
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT  
 AACAGTGAGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTTA  
 CCACGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTACAGACTACC  
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT  
 GGATGAAGTCATGAAGACCACCAAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGCTAG  
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGCGGAGTACAGTC  
 ACAGCCGCCCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGC  
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATTCT  
 ATGACCATATTAACCTACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGC  
 CTGGGGAACTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTACAGACCA  
 TACCAAGGACAAGGTACAGGAACTCAAATAT**TGA**CTCCCCTCCCCCAAAAAAATTATAAAAT  
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA  
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAAAATTTAAAGA  
 CAAAAAGTCAAAACA

**FIGURE 157**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT  
RRGLSEVPQGIPSNTRYLNL MENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS  
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY  
ISEGAFEGFLNLYLNLMCNKMDPNLTPLVGLEELEMNGHNFPEIRPGSFHGLSSLKKLW  
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSSLPHDLFTPLRYLVELHLHHNPWNCDCDILW  
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL  
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN  
ASAYLNVSTAELNTSNYSFFT TVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ  
TTRVPKQVAVPATD TTDKMQTSLDEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLKRKHQORS  
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE  
NSLGNLHPTVTTISEPYIIQHTTKDKVQETQI

[illegible]

**FIGURE 159**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV  
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD  
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD  
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLHSDGSKNFDGFHAIYEEITACSSSPCFHDG  
TCVLDKAGSYKACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV  
VSFFCNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH  
QLYSAAFSKQKLQSAPTCKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK  
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNE  
RTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD  
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSFGFKNDTLRSG  
VVSVDLSLLCEEQHEDHGI PVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR  
WHLMGLVSWSYDKTCSHRLSTAFTKVLPPKDWIERNMK

**FIGURE 160**

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA  
 AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAAC**ATG**GGC  
 TTCAACCTGACTTTCCACCTTTCCCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCT  
 GACAGTGGTTGGGTGGGCCACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCCCTAAAG  
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT  
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCCTTCTGTGTCTCCTTACCTCAG  
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC  
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC  
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT  
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT  
 TTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC  
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA  
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG  
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT  
 AACAACTACTGGGGATGGGGAGGCCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG  
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG  
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCACGAGTCTGG  
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA  
 TATCAACATCACAGTGGATTTCTGGTTTGGTGCA**TGA**CCCTGGATCTTTTGGTGATGTTTGG  
 AAGAACTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA  
 AGAACCTGTTACAGCTCATTTGTTGAGCTGAATTTTTCTTTTGTATTTTCTTAGCAGAGCT  
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG  
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT  
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT  
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT  
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCAATTTATCCTGTACAATCATCT  
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA  
 GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAG  
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCCAGGTATGCCT  
 TCCAGTGATGCCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGA  
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAATA  
 TGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA



**FIGURE 161**

MGFNLT FHLSYKFRL LLLLL TLCLTVVGWATS NYFVGAIQE I PKAKEFMAN FHKTLILGKGKT  
LTNEASTKKVELDNCPSVSPYLRGQSKLI FKPDLTLEEVQAENPKVSRGRYRPQECKALQRV  
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAE GKKFNRAKLLNVGYLEALKEEN  
WDCFIFHDVDLVPENDFNLYKCEEHPKHLVVG RNSTGYRLRYSGYFGGVTALSREQFFKVNG  
FSNNYWG WGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR  
VWR TDGLSSCSYKLVSV EHNPLYINITVDFWFGA

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites:**

amino acids 4-7, 220-223 and 335-338

**Xylose isomerase proteins:**

amino acids 191-201

**FIGURE 162**

CGTGGGCCGGGGTTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGCAGTTCTC  
GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCCGCA**ATG**  
GCCCAGGCAGTGTGGTTCGCGCCTCGGCCGCATCCTCTGGCTTGCCTGCCTCCTGCCCTGGGC  
CCCGGCAGGGGTGGCCGCAGGCCTGTATGAATCAATCTCACCACCGATAGCCCTGCCACCA  
CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG  
CCCGCTGACGCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA  
GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTTCGGCCACGTGCCCCGGGGAATTCCCGG  
TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG  
GTCCTCCCCATCACAGAGTTCCCTCGTGGGGGACCTTGTTGTCACCCAGAACACTTCCCTACC  
CTGGCCCAGCTCCTATCTCACTAAGACCGTCCCTGAAAGTCTCCTTCCTCCTCCACGACCCGA  
GCAACTTCCTCAAGACCGCCTTGTTTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG  
GTGACTGAAGACTCCGTGGTCTATTATACTATTCCATCATCGGGACCTTCACCGTGAAGCT  
CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGGCTGTGAAGCAGAAGA  
CCGGGGACTTCTCCGCTCGCTGAAGCTGCAGGAAACCTTCGAGGCATCCAAGTGTTGGGG  
CCCACCTAATTACAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCCTGGGGAGCCCTCC  
TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCTCCCGCTGGAGGAAGGGGAGTGCCACC  
CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTGGGGACTAC  
TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT  
GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA  
TGTTGGCCTTCATCATGTACATGACCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG  
AACCCGGAGCCACCCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCCTTTCTTGCT  
GGAGACTCCATCTGAGTACCTGGAAATTGTTCTGTGAGAACCACGGGCTGCTCCCGCCCCCTCT  
ATAAGTCTGTCAAACTTACACCGTGT**TCAG**CACTCCCCCTCCCCACCCCATCTCAGTGTTAA  
CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTTCAAT  
TGCGTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTCAGCCACTGCCACAAGCC  
CCTCCCTCTCTGTCAACCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA  
TAAGCCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT  
TTGATGCTTGGGGTGTTCCTGTGACTCCTAGGTGGGCCTGGCTGCCCACTGCCATTCTCT  
CTCATATTGGCACATCTGCTGTCCATTGGGGGTCTCAGTTTCTCCCCCAGACAGCCCTAC  
CTGTGCCAGAGAGCTAGAAAGAAGGTATATAAGGGTTAAAAATCCATAACTAAAGTTGTAC  
ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACA  
CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTTCAAGATGATCAGCTCTGTA  
TCTGGTTAAGTCGGTTGCTGGGATGCACCCTGCACTAGAGCTGAAAGGAAATTTGACCTCCA  
AGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCAGTTCTTGC  
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT  
AATACTGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTG  
AACTTTCACTGAGGAAAAGGCCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGG  
TGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA  
GATCGAGACCACCCTGGCTAACACGGTGAACCCCGTCTCTACTAAAAAATACAAAAAGTT  
AGCCGGGCGTGGTGGTGGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG  
GTGCGAACCCGGGAGGCGGAGCTTGCACTGAGCCCAGATGGCGCCACTGCACTCCAGCCTGA  
GTGACAGAGCGAGACTCTGTCTCCA

**FIGURE 163**

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA  
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF  
VVLPITEFLVGDLVVTQNTSLPWPSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ  
MVTEDSVVYYNYSIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL  
GPTLIQTFQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTFRDPGD  
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV  
ENPEPPSGVRCCCQMC CGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 339-362

**N-glycosylation sites.**

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

**FIGURE 164**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCT  
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA  
CAACAGACGGGACAACCTTGCAGAGCTGCAACCCCAGGACAGAGCTGGAGCCAGGGCCAGCTG  
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCT  
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTG  
CCCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA  
TGGCTGGTTCTTTTGTTTTCCAAA  
AAA

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**FIGURE 165**

MALSSQIWAACLLLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH  
FPICIFCCGCCHRSKCGMCCKT

09974460

**FIGURE 166**

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC  
 CTGGATCTTCCACC**ATG**TTTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC  
 ATCTCCCTGACTGTCTCTTACCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG  
 AGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA  
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC  
 GGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTGGAAGTGG  
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC  
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG  
 GAGTCCTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC  
 GGTCTGTGGGGGTTAGGAGTGCTGATTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC  
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT  
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG  
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT  
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGCCAGCGATGGCTATTATGCC  
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTGAGAGAGCCATGGTGAAGGCCTG  
 CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA  
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC  
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTACCC  
 TGTTGCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGA  
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG  
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAAATCTGC  
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGG  
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCAC  
 AAGGACAGGAGCCGCTCC**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA  
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCACTGCTGTGTCTTTCCAGACTCCAGGG  
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGCAGCGGGATCCCTGT  
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA  
 CGAGATGCCTTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA  
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT  
 GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG  
 CTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGC  
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTCAGCAAAATG  
 AAGGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG  
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTCTGACTCCAGGCTAACCCTGAACTCCCC  
 ATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG  
 GAATGGTGGTGATTCCCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGA  
 AGGACACATCACGTTCAAGTACAGGCCCAAAAACGGGGCACGGCAGGCCTGAG  
 CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA  
 TGA



**FIGURE 168**

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA  
CGTCTCCTCCAGGGATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC  
ACCTGGCAGGCCCAGGCTGTTCCCACCATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGA  
CGATACCTATGTGGGTGTGTCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG  
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC  
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT  
CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG  
GCTCCCGGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGG  
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG  
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT  
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCGGGGCTGT  
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG  
GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTTGGGCCC**TGA**AAGTCCA  
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG  
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACCCAGG  
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTATGTGATGGGGACTTCCT  
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTTGCAATGTGGAGACA  
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA



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**FIGURE 169**

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH  
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSREL  
YMRHFPPFKALHFYLIRALQLLRGSGGCSRGPGEVVFRRGVGSLRFEPKRLGDSVRLGQFASSS  
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLLAPGEFQLSGVGP

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**FIGURE 171**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT  
IQEGGTIIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQOPSTQEYVLHV  
YEHLSPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW  
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW  
FLKRERQEEYIEKKRVDICRETPNICPHSGENTHEYDTIPHTNRTILKEDPANTVYSTVEIP  
KKMENPHSLLTMPDTPRLFAYENVI

**FIGURE 172**

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC  
TCTGGACCCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC  
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC  
AGCCAGAAGGGGGCCTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA  
GATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAGAAGAATGACTCAGGGATCTACTATGT  
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG  
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG  
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT  
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG  
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAGCAGAACTTCTCAAGCCCC  
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCT  
GTGTCTCCTGTTGGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC  
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCTGGGAA  
ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA  
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAA  
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAG  
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 173**

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAA**ATGA**AAGATGCTGCTGCT  
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA  
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA  
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGAGAGAA  
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG  
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT  
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA  
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA  
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT  
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC  
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC  
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC  
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT  
TTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

[illegible]

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**FIGURE 175**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACC**ATG**ACCTGCTGCGAAGGATGGACATCCTGCAA  
TGGATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG  
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC  
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG  
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA  
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC  
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA  
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG  
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC  
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT  
TGTTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC  
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTG**TAG**TTTAATGGGAATAAAATGTAAGTA  
TCAGTAGTTTGAAAAAAAAAAAA

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**FIGURE 176**

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA  
IPATTMSLTARKKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNA  
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL  
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

FOR "E94660"



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GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT  
 GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT  
 GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC  
 CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG  
 CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTGAA  
 AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC  
 CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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**FIGURE 178**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV  
KHCTDQISFKKRLSLKKSWWK

TOPP "E32660

**FIGURE 179**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG  
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG  
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTC  
GAACTGTGAC**ATG**GAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG  
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG  
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG  
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC  
TCATCACTCCAGGCTCTGCCACTACTTGCT**TGA**GACACAGGACTGGCCTCCAGGGATGGCCTGA  
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC  
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG  
CCCCACCACCCCCTCA



**FIGURE 181**

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCC  
TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC  
CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCC  
AGTGTTTCCCACAGCCCCCAAACGGAACTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT  
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGCCACCTATTCCCAGGGCTTTACGGT  
ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA  
CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG  
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC  
GCCCGCCTTCCATTTCAACATCCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACA  
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG  
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG  
TCAGGAGAGGCCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA  
GAAGCCAGCATATCCTCCAGCACATGGACTTCTGTATTACCTCTCCCATGACGGGCGGGCGC  
TTCCACAGGGCCTGCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCTG  
CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG  
ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT  
ATAAGAGCAGAGGCTGACACCTTCATGTTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC  
CTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC  
AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCC  
TTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCG  
ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC  
TCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGAC  
CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCTC  
CGCAGGGCCCAGGAACTGCATCGGGCAGGCGTTCCGCATGGCGGAGATGAAAGTGGTCCTGG  
CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAA  
TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCA  
GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAAA



**FIGURE 183**

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC  
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA  
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA  
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG  
AAAGCAGACTCAAGTACCAACATTTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT  
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA  
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT  
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAC  
AGTGTGGAGAAAAACTAGGCCAACTACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT  
ATGTTTTGCACAAAAAAAAAAAAAAAAA

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**FIGURE 184**

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA  
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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**FIGURE 185**

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT  
GGGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA  
CCACCTCCGCCAGGAAGTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC  
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT  
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA  
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGA  
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT  
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG  
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGCCTTACTCACCTCTCTCT  
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA  
CAAGCTCAGGAGGCGAATAAATGTTCAAAGTGT

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**FIGURE 186**

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG  
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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**FIGURE 187**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC  
GTGAACCCCGGGTGCTCCGCACGGACCCAGATGTCAAGAAT**ATGA**ACACGTGGCTGCTGT  
TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG  
CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT  
GAGTATGTCCCCACCCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC  
TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT  
GTCCCCCGTGTGCGCATGTGTTTCCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAAA  
GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC  
TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCT**TGA**AGTAACAAGTTTAAATGTTTCTCAGA  
GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT  
CCAAAAACACAAGTAGAAATTCTAACAAATGAAATATATTACAGGCAGGTACCCACTAACCA  
AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTCTC  
AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT  
AACAAACAACCTCCCTGCTCCTGGCACCCAGCCGTTTTTGGTTCATGGTGGGCCAGCTGCAAAGCG  
TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC  
ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA  
ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTCTCAGGCTCTGGGCTCACCTCCATCTCCAGA  
GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA  
GCCTCCTTGTTTATAACCACAGGTTACCCTACAAACCACTGTCCCCACACAACCCTGGGGAT  
GTTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA  
ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 188**

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLSPRS PQGW  
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ  
AQQEAELTPRPAGVVPGA

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TOSTT-EE9/6650



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**FIGURE 190**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWVFGTQKVPKPLCEKGLAAKCFDMP  
VSLDGD TNTSTQEVVQYNWETGDDRF SFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR  
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL  
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRL ETTCLE  
LWLGLLHGLALLHLLHGVGCHHLQHVVHVDGAGVQVQA

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AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTTGGTTACCCCTTGGTCTCCTG  
TCTTTATGTCTTTCTCCTCTTCCTATTCTGTGCATCTCCCTCACTTAAGTCTCAGGCCTGTCA  
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG  
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT  
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG  
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCCTCCCAA  
GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG  
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT  
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTTCAG  
GACATTGCCCCCTGTGTGCCACCAAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCT  
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT  
ATGGCGATGGCCATGATGTTACAATCCCCTTGCCTGAATAATCAAGTGGGAAGGGGAAGCA  
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAA  
GGGAAGCAACAGGAACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC  
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA  
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG  
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG  
AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC  
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME  
HRNHLCFCDLYDRATSPPLKCSLL



**FIGURE 193**

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGTGGAGCCAGGAGCGACGTCA  
 CCGCC**ATPG**GCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTT  
 GGATGTGCCCTTCCAATATACAACAAATACTGGCCCCCTTTTGTCTATTTTTTTACATCCTTTACCTATTCC  
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAACTTGCCATCTTTC  
 TTACAACGGGCATTGTCGTGTCAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGA  
 GCTTGTGCACTTGTCTCACAGGAAACACAGTCATCTTGAACCTATACTAGGCTTTTTCTTGGTCTTTGGAAG  
 CAATGACGACTTCAGCTGGCAGCAGTGG**TGA**AAAGAAATTAAGTAAGTATTGTCAAATGGACTTCCTGTCATTT  
 GTTGGCCATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTA  
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGCTGAAGGATTAAAGGATTTTCT  
 CTTTTGGAAAAGCTTGACTGATTTTACACTTATCTATAGTATGCTTTTTGTGGTGTCTGCTGAATTTAAATAT  
 TTATGTGTTTTTCTGTTAGGTTGATTTTTTTTGAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA  
 TTTGCATTGGTTAGGAATTCAGAATTCGCCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATTTAT  
 TAGCCTCCATTATTACAAAAAATTATAAAAAATAAGTTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG  
 CAGACATACAGACGGTTGGCATACTGTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG  
 GGGCCAAGTGTTAATGCCATGCCCTCCGTTAAGGGTGTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG  
 AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGAATTTATGTTAAACTTTA  
 AGGTAAGGGTGTA AAAACATTTTGGAGATAAGGTTTTATTATGTTTATTATTGTTAGAGTGAGTTGCAATGT  
 GGGAAGAAATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTATATAAGTGAAATTTGTGATCTCCTATC  
 AACCTTTTCATGTTTTACCCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGC  
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCTCTTTTGAATTATTTGGTATGTTGTATATATTACATAAAA  
 TAACTTTTCAAATATAGTTTAAATAACACTTAGAAGTGTTTACTTACCTGGAAAATAATTGCTATGCCGTACATT  
 CAGAGTGCCCCCTCCCTGCAAGGCCTTGCCATGATTAACAAGTAACTTGTTAGTCTTACAGATAATTCATGCA  
 TTAACAGTTTAAGATTTAGACCATGGTAATAGTAGTTCCTATTCTCTAAGGTTATATCATATGTAATTTAAAG  
 TATTTTAAAGACAAGTTTCTGTATACCTCTGAAGTGTGTTTTGAGTTCATCATGATAGATCTGCTGTTT  
 CCTTATAAAAGGCATTTGTTGTGTGAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT  
 ACCTGACCAAAAAATTCAGTAACAGGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTATCAGGA  
 CTTTTTTTCAGGAGTGGGTTATAAAAAACATTCAGTTGGTCTGACAGTATTTTGTTAAGGATATTTGTTTGTATG  
 TTTATTCAGTATACTTACATAAAAAATTATTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGT  
 TTTATGAAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTTGTTCAGCTTTTTTACTAAAGATGCCTAA  
 AGCCACAGGTTTTATTGCCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG  
 GCGTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGGCTTGTGGTATTATAATGTTTCAGATTTCAAGAGGAA  
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTGTGCTTGTGATCTACTGGACTTT  
 TTTTTTGCAGGAAGTGCAATCTCTGGTCTTCCCTATTTTCTGTTCTGGATGTCAGTGCAAGTGCACTGCTACTG  
 TTTTATCCACTTGGCCACAGACTTTTTCTAACAGCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCATT  
 GTGCTTTTGACCTTGTATACTAGCTTGACATAGTGCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT  
 TTTCCATAGAATATGCACTGATACAACATTACCATTCTTCTATGGAAAGAAAACCTTTTGATGATGAAACAATAA  
 AGATTTTAAATACTATTTTAAAAA

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**FIGURE 194**

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLEVLFYILSPIPYCIARRLVDDTDAM  
SNACKELAIFLT TGIVVSAFGLPIVFARAH LIEWGACALVLTGNTVIFATILGFFLVFGSND  
DFSWQQW

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[illegible]

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**FIGURE 196**

MDFLLLGLCLYWLLRRPSGVVLCILGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH  
NLSGLLGLSLRYNSLSELRAQQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ  
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIQDCRS  
LKFLDIGYNQLKSLARNSFAGLFKLTEHLHNDLVKVNFAHFPRILISLHSLCLRRNKVAIV  
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT  
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSG  
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA  
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQAAMSAQEYYVDYKPNH  
IEGALVIINEYGSCTCHQQPARECEV

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**FIGURE 197**

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC  
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTTCGAGCCAA  
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCGCCGTTGAGTTCCCGGCGGACAAGATGG  
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA  
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG  
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT  
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC  
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGGCCCTGGCGCTAG  
CCCCGTGCGTGTCGCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG  
CTGTTTTCTGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGCCGGGCGCGCTGAGCGTG  
GGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG  
GATCTGCGCGGCCCTGCTCCAGCCCCCT

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**FIGURE 198**

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE  
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA  
PGLFFVDAERVPCRHDDVFFPPSASFVRVGLGPGASPVVRVSISALGRFTFTRDEDLAVFLASR  
AGRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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**FIGURE 199**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTT  
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTT  
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCA  
TTGACGTGGTACAGCCTTTCCTTCATACCATTTGCAAGGGATGCTGTGAAGAAGTGTGTTGC  
CGTGTGTCTTGCATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAG  
CTGGTGGACAGTTTTGTAACCTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT  
TGCAGCAATGTGTTGCTTGTGATTCGAACATTTGAGGGTTACTTTTGGAAGCAACAATACAT  
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA  
TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCCTGAATTCCTCATGAATACAAAC  
CTATTCAGCAACAGCAA  
AAAAAAAAAAAAAAAAAAAAAAAAA





TTGAGCGCAGGTGAGCTCTCTGCGGTTCCGGGGGCGTTCTCTCCAGTACCCTCCCGCGGTACC CGCGGCGCGC  
CCGAGGGAGTCTCTCCAGACCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT  
GGGAGAGAAAAATTAGGGGGAGAAAAGGACAGAGAGCAACTACCATCCATAGCCAGATAGATTATCTTACACTG  
AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTGTCTTTCATACTTGGCTGCACTGAGTCTTTC  
AACCACCTTTTCTCTCCAAC TAGACCAGCAAAGGTTCTACTAGTTTCTTTTGTAGGATTCCGTTGGGATTACT  
TATATAAAGTTCCAACGCCCCATTTTCATTATATTATGAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT  
TTTATTACAAAACCTACCCTAACCATTATACTTTGGTAAGTGGCCTCTTTGCAGAGAATCATGGGATTGTTGG  
AAATGATATGTTTGATCTTATTCGGAACAAATCTTCTCTTGGATCACATGAATATTTATGATTCCAAGTTTT  
GGGAAGAAGCGACACCAATATGGATCAAAAACGAGGGGAGGACATACTAGTGGTGCAGCCATGTGGCCCGGA  
ACAGATGTAAAATACATAAGCGCTTTCCTACTCATTACATGCCTTACAATGAGTCAGTTTCAATTTGAAGATAG  
AGTTGCCAAAAATGTTGAATGGTTCAGTCAAAAGAGCCCAATAATCTGGTCTTCTCTATTTGGGAAGACCTG  
ATGATATGGGCCACCAATTTGGGACCTGCAGTCCGCTCATGGGGCTGTCAATTCAGATATTGACAAGAAGTTA  
GGATATCTCATACAAATGCTGAAAAAGCGAAAGTTGTGGAACACTCTGAACCTAATCATCACAAGTGATCATGG  
AATGACGCAGTGCTCTGAGGAAAGGTTAATAGAACTTGACCAGTACCTGGATAAAGACCACTATAACCTGATTG  
ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAGGTAATTTGATGAAGTCTATGAAGCACTAACTCACGCT  
CATCTTAATCTTACTGTTTACAAAAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCAAGTTCA  
ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACAATTTTACAGAATAAGTCAGATGACTTCTGTGGAAC  
ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAAGCCATGGTCTGCTTTCAGAAAGAATTT  
TCAAAAGAACCCATGAACCTCCACAGATTTGTATCCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCA  
CAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTGAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA  
CTATACTCCTCCCTGGTAGTGTTAAACCAGCAGAATATGACCAAGAGGGGTCAATCCCTTATTTCAAGGGGT  
TCTCTTGGCAGCATTATAGTGATTGATTTTTTTGTAATTTTTCATTAAAGCATTTAATTCACAGTCAATACCTGC  
CTTACAAGATATGCATGCTGAAATAGCTCAACCATATTATACAAGCCTTAATGTTACTTTGAAGTGGATTTCATA  
TTGAAGTGGAGATTCCATAATATTTGACGTGTTTAAAGGTTTCAAATCTGGGAAACCAAGTTCCAAACATCTGC  
ATGAACCATTAAGCAGTTAATATTTAGGTATACACACACACACACACACATACACACACACGGACCAA  
ATACCTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGTCTCCATTGTTCACTGTAGCATAGGGATAGATAAG  
ATCCTGCTTTATTTGGACTTGGCGCAGATAATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTTAT  
ATTGCACTTTTAAATTTCTCTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAAC  
TTGATTGAAAATGACAACTTTTGCACCAATGTACAGAATACTTGTACGATTTGTTCAAAGTGAAGGAAAT  
TCTAATAATCCCGAATAATGAACATAAGAAATCTATCTCCATAAATTGAGAGAAGAAGAAGGTGATAAGTGTGA  
AAATTTAAATGTGATAACCTTTGAACCTTTGAATTTTGGAGATGTATTCCCAACAGCAGAATGCAACTGTGGGCAT  
TTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTCATTTATTTTTCCCTCAAAGAGAGTCAAATACTGACAG  
ATTGCTTCTAAATATATTGTTTCTGTCATAAAATTTATTGTGATTTCTGATGAGTCATATTACTGTGATTTTCA  
TAATAATGAAGACCAATGAATATACTTTCTCTTATATAGTTTCAGCAATGGCCTGAATGAAGCAACAGGCA  
CCATCTCAGCAATGTTTTCTCTTGTGTTTGAATTTATTTGCTCTTGGAAATTAATCACTATTATTAATCATTA  
AAATCAAATTTGGATAAAAAA

**FIGURE 202**

MTSKFILVSFILAALSSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK  
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIW  
ITNQ RAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY  
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITS DHGMTQCSEER  
LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTAHPNLT VYKKEDVPERWHYKYN  
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD  
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF  
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

**FIGURE 203**

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAGTGC GGGAGGCCAG  
GACAGGCCCCACCCTGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGC  
AGAGAGGCCAAGCCCCCTTGCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA  
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC  
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA  
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG  
AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCC  
CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT  
CAGCTCCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC  
TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG  
GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT  
ATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG  
TGGTCTCATTATCCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC  
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT  
TAAGACACGTTTCAAGACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA  
AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCTGGACTGATGAGTTTGCTGTATC  
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT  
CACACAGCCACCGTGAAAGTCCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG  
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA  
TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC  
AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 204**

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYYKKWENEEEEEEEEQPPPTPV  
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILD  
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSFTTSLRSWMPVVVVVSFILDI  
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS  
CSEKPLD

**FIGURE 205**

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCAACAT  
 GCTCTGTCTGTGCCTGTACGTGCCGGTCATCGGGGAAGCCCAGACCGAGTTCCAGTACTTTG  
 AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCCCTCC  
 CAGGAATTCTCCACCTACCGCCAGTGGAAAGCAGAAAATTGTACAAGCTGGAGATAAGGACCT  
 TGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGA  
 GGCTGGTGTTTAAGATTTTGGACAAAAGAATGATGGACGCATTGACGCGCAGGAGATCATG  
 CAGTCCCTGCCGGGACTTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTTCTCAAGAG  
 CATGGATAAAAAACGGCACGATGACCATCGACTGGAACGAGTGGAGAGACTACCACCTCCTCC  
 ACCCCGTGGAAAACATCCCCGAGATCATCCTCTACTGGAAGCATTCCACGATCTTTGATGTG  
 GGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGGGGATGTGGTG  
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGG  
 ACAGGCTCAAGGTGCTCATGCAGGTCCATGCCTCCCGCAGCAACAACATGGGCATCGTTGGT  
 GGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGCAATGGCATCAA  
 CGTCCCTCAAAATTGCCCCGAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC  
 TTGTTGGTAGTGACCAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCTTTGGCA  
 GGGGCCATCGCCCAGAGCAGCATCTACCCAATGGAGGTCTGAAGACCCGGATGGCGCTGCG  
 GAAGACAGGCCAGTACTCAGGAATGCTGGACTGCGCCAGGAGGATCCTGGCCAGAGAGGGG  
 TGGCCGCTTCTACAAAGGCTATGTCCCCAACATCTGGGCATCATCCCCCTATGCCGGCATC  
 GACCTTGCAGTCTACGAGACGCTCAAGAAATCCCTGGCTGCAGCACTATGCAGTGAACAGCGC  
 GGACCCCGGCGTGTGTTGTGCTCCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGG  
 CCAGCTACCCCTGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGCT  
 CCGGAGGTGACCATGAGCAGCCTCTTCAAACATATCCTGCGGACCGAGGGGGCCTTCGGGCT  
 GTACAGGGGGCTGGCCCCAACCTTCATGAAGGTTCATCCAGCTGTGAGCATCAGCTACGTGG  
 TCTACGAGAACCTGAAGATCACCCCTGGGCGTGCAGTCGCGGTGACGGGGGGAGGGCCGCCCG  
 GCAGTGGACTCGCTGATCCTGGGCCGAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATG  
 TGCCAACACTAAGCTGTCTCGAGCCAAGCTGTGAAAACCCTAGACGCACCCCGAGGGAGGGT  
 GGGGAGAGCTGGCAGGCCCAGGGCTTGTCTGCTGACCCCAGCAGACCCTCCTGTTGGTTCC  
 AGCGAAGACCACAGGCATTCTTAGGGTCCAGGGTCAGCAGGCTCCGGGGTCCATGTTGTA  
 GGACAGGACATTTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGCTTAGT  
 TCTTCCATTTACCCCTTGCAGCCAGCTGTTGGCCACGGCCCCCTGCCCTCTGGTCTGCCGTGC  
 ATCTCCCTGTGCCCTCTTGTGCTGCCTGTCTGCTGAGGTAAGGTGGGAGGAGGGCTACAG  
 CCCACATCCCACCCCTCGTCCAATCCCATAATCCATGATGAAAGGTGAGGTACGTGCCCT  
 CCCAGGCCTGACTTCCCAACCTACAGATTGACGCCAAGCTTGGCTGTGAAGGAAGAGGAAAG  
 GATCTGGCCTTGTGCTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT  
 TGGGAGTGCAGGGGGCTCGGGCTGCCTGGCCTGGCTGCACAGAAGGCAAGTGCTGGGGCTCA  
 TGGTGTCTGAGCTGGCCTGGACCTGTGAGGATGGGGCCACCTCAGAACCAACTCACTG  
 TCCCCACTGTGGCATGAGGGCAGTGGAGCACCATGTTTGAGGGCGAAGGGCAGAGCGTTTGT  
 GTGTTCTGGGGAGGGAAGGAAAAGGTGTTGGAGGCCTTAATTATGGACTGTTGGGAAAAGGG  
 TTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG  
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCTGTCCAACC  
 CCAGCAGGGGCGCAGCGGGACCAGCCCCACATTCCACTTGTGTCACTGCTTGGAACTATTT  
 ATTTTGTATTTATTTGAACAGAGTTATGTCCTAACTATTTTATAGATTTGTTTAATTAATA  
 GCTTGTCATTTTCAAGTTCATTTTTTATTCAATTTATGTTTATGTTTATGTTTATGTTTATG  
 AAGCCCGCCAGTGGGATGGGAGGAGGAGGAGGAGGGGGGCTTGGGGCGCTGCAGTCACAT  
 CTGTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAAGGCAGCAGCCCTG  
 GCTCCTTTCTTTTGGCAGGTGGGGAAAGGGCTTGGCCCCAGCCTTAGGATTTACAGGGTTTGA  
 CTGGGGGCGTGGAGAGAGAGGGAGGAACCTCAATAACCTTGAAGGTGGAATCCAGTTATTTT  
 CTGCGCTGCGAGGGTTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAGTGAGGTGCCTCT  
 CACTGTGAATTTTGTGGTGGGCGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCCGTCCCTCC  
 CAGCCTTCTGCTGCCCTTGTCTTAACAATGCCGGCCAAGTGGCGACCTCACGGTTGCACTTCC  
 ATTCCACCAGAATGACCTGATGAGGAAATCTTCAATAGGATGCAAAGATCAATGCAAAAATT  
 GTTATATATGAACATATAACTGGAGTCGTCAAAAAGCAAATTAAGAAAGAATTGGACGTTAG  
 AAGTTGTCAATTTAAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAA  
 AA

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## **FIGURE 206**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD  
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK  
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW  
WRHLVAGGGAGAVSRTCTAPLDRLKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI  
NVLKIAPESAIFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMAL  
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNS  
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG  
LYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Transmembrane domain:**

amino acids 284-304, 339-360, 376-394

#### **Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

#### **N-glycosylation site.**

amino acids 129-133, 169-173

#### **Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140



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**FIGURE 208**

MASLGQILFWSIISIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI  
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD  
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFQPTVVWASQVD  
QGANFSEVSNTSFELNSENVTMKVVSVLNVTINNNTYSCMIENDIAKATGDIKVTSEIKRR  
SHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

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[illegible]

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**FIGURE 210**

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLLQEMKTLFLNTEYLMPEFL  
LNQCGSLLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS  
RHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

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CTTCTGTAGGACAGTACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG  
GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTTCGAAAAGATTCCGCAATAAAACT  
TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT  
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACC**ATGA**AGGGGCATCCTCG  
TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT  
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG  
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT  
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT  
GCTGAAGAACACTTTCATTTTGTAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG  
CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG  
AATCTAATGGAACCTCCTGTTCGTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTC  
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC  
CAACGTCAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCA  
TCTTTCGAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT  
TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG  
GGGACTGCTGCCC**TGA**AGGTCCTGGGGCTGCACTTTGCCCAGCACCCCATTTCTGCTTCTCTG  
AGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTTCCCTGCTCTGCCCCGTTTAACTGC  
CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA  
AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 212**

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLETPVR  
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE  
CPACYESNGTSCRGKPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVS NATCQFLSGENK  
TLGGVIFRKFE CANVNSLTPTSAPT TSHNVGSKASLYLLALASLLLRGLLP

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**FIGURE 213**

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA  
GGGCTTGCCTCACTGGCCACCCTCCCAACCCCAAGAGCCCAGCCCC**ATG**GTCCCCGCCGCCG  
GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCCTG  
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCAG  
CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA  
ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC  
ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA  
GGGGGTGTGATTAATGCCGGAAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCAGACTCCCA  
ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG  
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC  
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTACCCTCACCCACAG  
CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC  
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT  
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGACCTATCAACAATGTC  
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT  
GCCTCTCAGAGCACCACCAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG  
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTTGGAAACGGGTCA  
GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA  
GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT  
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTGTAGTACAGAAAAACAAAAGTGGAAAA  
CACAA

MVPAAGALLWVLLLNLGPRAGAAGLTQTPTMQRVSLRFGGPMTRSyrSTARTGLPRKTRI  
 ILEDENDAMADADRLAGPAAAEALLAATVSTGFSRSSAINeedGSSEEGVVINAGKDSTSREL  
 PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP  
 SPSPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC  
 TYQQCPCNRLREECPLDTSLCDTNCAStTSTRTTTTPFPTIHLRSSPSLPPASPCPALA  
 FWKVRIGLEDIWNSLSSVFTEMQPIDRNQR

**FIGURE 215**

CCCGGGTGACCCACGCGTCCGGGGAGAAAGG**ATG**CCCGGCCTGGCGGCGCGGTTGGTCTGCTAGCTGGGGCA  
 GCGGCGCTGGCGAGCGGCTCCAGGGCGACCGTGAGCCGGGTACCAGCGACTGCGTACTGCAGTGCGAAGAGCA  
 GAACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT  
 GTCGGGACGACTGTAAGTATGAGTGTATGTGGGTACCGTTGGGCTCTACCTCCAGGAAGGTACAAAGTGCCT  
 CAGTTCCATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCGTTTCT  
 CAATGGCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACA  
 CCTGTGTGGCCTTCGCCTGGGTGTCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGAC  
 CTCACAGAGAAAATGGACTACTTCTGTGCCTCCACTGTATCCTACACTCAATCTACCTGTGCTGCGTCAGGAC  
 CGTGGGCTGCAGCACCAGCTGTGGTCAGTGCCCTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCT  
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG  
 GTGTGGTGGCTGGCCTGGTGCCTGTGGAACCAGCGCGGCTGCCTCACGTGCGCAAGTGCCTGGTGGTGGTCTT  
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCCACCGCTCTTCTGGGTCTGGATGCCCATGCCA  
 TCTGGCACATCAGCACCATCCCTGTCCACGTCCTCTTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG  
 AAGGAATCAGAGGACAAGTTCAAGCTGGACT**TGA**AGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCC  
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAAGTGGACATGA  
 AGGATGTGGGCCCAGAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG  
 AAGGCCCTCCAGCATCTGGGACTCGAGAGTGGGCAGCCCTCTACCTCCTGGAGCTGAAGTGGGGTGGAACTGA  
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCTGTTCTCTCCCAACAGCCTCCTCCCCACATCCCCAGCTG  
 CCTGGCTGGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGGACACAGGCCTTAGGGATACAGGGGGTCCC  
 CTCTGTTACCAACCCCCACCCCTCCTCCAGGACACCACTAGGTGGTGTGCTGGATGCTTGTCTTTGGCCAGCCAA  
 GGTTACGGCGATTCTCCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTACCCTGACC  
 GTTGCCCTAGCCAGGTTCCAGGAGGCCCTCACCATACTCCCTTTTCAAGGCCAGGGCTCCAGCAAGCCCAGGGCA  
 AGGATCCTGTGCTGCTGTCTGGTTGAGAGCCTGCCACCGTGTGTGGGAGTGTGGGCCAGGCTGAGTGCATAGG  
 TGACAGGGCCGTGAGCATGGGCCTGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTTGT  
 CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTGAGGGGGTGGGTGTGTAGCGTGGGTTAGGGGAACGTGTG  
 TGCGCGTGTGGTGGGCATGTGAGATGAGTGACTGCCGGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT  
 GAGGGAATCCTGTACCATCAATAACTTGTGGAGCGCCAGCTCTGCCCAAGACGCCACCTGGGCGGACAGC  
 CAGGAGCTCTCCATGGCCAGGCTGCCTGTGTGCATGTTCCCTGTCTGGTGCCCTTTGCCCGCTCCTGCAAAC  
 CTCACAGGGTCCCCACACAACAGTGCCCTCCAGAAGCAGCCCTCGGAGGCAGAGGAAGGAAAATGGGGATGGC  
 TGGGGCTCTCTCCATCCTCCTTTTCTCCTTGCCTTGCATGGCTGGCCTTCCCTCCAAAACCTCCATTCCCCCT  
 GCTGCCAGCCCCCTTGGCATAGCCTGATTTTGGGGAGGAGGAAGGGGCGATTTGAGGGAGAAGGGGAGAAAGCT  
 TATGGCTGGGTCTGGTTTCTTCCCTTCCCAGAGGCTTACTGTTCCAGGTTGGCCCCAGGGCAGGCAGGGGCC  
 AACTATGCCGTGTGCCCTGGTAAAGGTGACCCCTGCCATTTACCAGCAGCCCTGGCATGTTCTGCCCCACAGG  
 AATAGAATGGAGGGAGCTCCAGAACTTTCCATCCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGTG  
 CTCTGCCCCTGACCCCTTGTCCCTCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTG  
 GCCTGCGCTAGCTTCTTTTGATACTGAAAACCTTTAAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAA  
 TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

**FIGURE 216**

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW  
TCRDDCKYECMWVTVGGLYLQEGHKVPQFHGKWPFSRFLFFQEPASAVASFLNGLASLVMLCR  
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR  
TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR  
RLPHVRKCVVVVLLQLGLSLLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL  
KESEDKFKLD

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

**N-glycosylation site.**

amino acids 40-44

**N-myristoylation site.**

amino acids 43-49

**CUB domain proteins profile.**

amino acids 285-302

**Amiloride-sensitive sodium channels proteins.**

amino acids 162-186



**FIGURE 217**

[illegible]

**FIGURE 218**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEEL  
DAEVLEV FHP THEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGRDLINTN  
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV  
RLINKFNSSSSSLEEKIAALFDLEYVHQM DNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF  
VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL  
GGLQVLRTL VQEKGTEVLAVRVVTL LYDLVTEKMFAEEEAELTQEMSPEKLQQYRQVHLLPG  
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCDRDRYRQDPQLGRTLASLQAEYQVLAS  
LELQDGEDEGYFQELLGSVNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340

**FIGURE 219**

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCC  
 CTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCTCGTGGGGTCGCGTTGCCACCCCA  
 CGCGGACTCCCCAGCTGGCGCGCCCCTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCC  
 TTCCCACCTGACCAGCC**ATG**GGGGGTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTCCGGC  
 CCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGT  
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGG  
 TCCATGTGACCGACCGGTACAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCT  
 GTCTCTGTCCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA  
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT  
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT  
 GATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCCCTATTACTTCCTGACTTC  
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG  
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCTGGTGGTTGGGAGTCACCTACTGACATCG  
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT  
 TTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCC  
 TCTTGTGTAAGGAC**TGA**CTACCTGGACTGATCGCCTGACAGATCCCACCTGCCTGTCCACTG  
 CCCATGACTGAGCCCAGCCCCAGCCCGGGTCCATTGCCACATTCTCTGTCTCCTTCTCGTC  
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT  
 TACCAGGAGCAGCCTGGGTTCAGCCAGTCAGTACTGGTGGGTTTGAATCTGCACTTATCCC  
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTCACTGCTCTGCTCTCAC  
 CCTGCCCAAGACTCACCTCCCTTCCCCCTCTGCAGGCCGACGGCAGGAGGACAGTCGGGTGAT  
 GGTGTATTCTGCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC  
 CTGGGGTGCCCTCCTGATGTCCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAG  
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA  
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC  
 AGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCCTAAACTGCCTTTTTTTCTTTTTT  
 GAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTCTCTAACCTCCTTGGGCTATATTTCTC  
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTTCGGTCCCTTTCTCCTTGGTCCCAGACCTT  
 GGGGGAAGGAAGGAAGTGCATGTTTGGGAACCTGGCATTACTGGAACATAATGGTTTTAACCT  
 CCTTAACCACCAGCATCCCTCCTCTCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGC  
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGG  
 GAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGT  
 ATCATTTTCTGCTGAGGGTGGAGTGCCCATCCTTTTAATCAAGGTGATTGTGATTTTGA  
 AATAAAAAAGAATTTGTAAAAA  
 AA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 220**

MGA AVFFGCTFVAFGPAFAFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR  
SDARLQYGLLI FGA AVSVLLQEVFRFAYYKLLKKADEGLASLSE DGRSPISIRQMAYVSGLS  
FGIISGVFSVINILADALGPGVVG I HGDS PYYFLTSAFLTAAIILLHTFWGVVFFDACERRR  
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

PDB ID: 1Z65B

**FIGURE 221**

AAGCTGGTTTAAAGGAAGCAGAGGAGGGTTAGATTCGTTGAGTGAGGACGGAAGATCAACCCA  
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT  
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC  
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

**FIGURE 222**

GACCGACCGTTCAGATGCCCCGGTTCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG  
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG  
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN  
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTTGGNTGATGCAN  
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAATTCCTGAATTCAGCCTTT  
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA  
GAGGAG

**FIGURE 223**

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTCCCTTTCCCCG  
GGGTCTGGGGTGACATTGCACGGGGCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC  
CCAGNTGGNGCGCCCTTCCCATTTCCTGTCTGGTCAGGCCCCACCCCCCTTCCCACNTG  
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTTCGGCCCGGCCTTCG  
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCA'GGGGCA  
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC  
CGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCC  
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA  
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG  
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTTG  
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

**FIGURE 224**

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTCCCCGGGG  
TCTGGGGGTGACATTGCACCGCGCCCNTCGTGGGGTTCGCGTTGCCACCCACGCGGACTCCC  
CAGNTGGCGCGCCCCCTCCCATTTGCCTGTCTGGTTCAGGCCCCCACCCCCCTTCCACCTGA  
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTTCGGGCCCGGCCTTC  
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGC  
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGA  
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC  
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT  
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG  
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTT  
GGGCCAGGTGTGGTTGGGATCCATGGAGAC



GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAG  
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC  
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG  
 TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCTCCTTGCCCTGTCTGGAGGCTGCT  
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT  
 CCTTGTGGTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCC  
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT  
 CTCGCCAACAAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA  
 GGACCTGGGAGCTGGGGCCGGGGAAGACGCCCCGGTCGGATGACAGCAGCAGCCGCATCATCA  
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC  
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCACTGCAG  
 GAAGAAAGTTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGC  
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCCACCTGGCTACTCCCACCCTGGCCACTCT  
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTCGTCCCCTAAAGATGTCAGACCCAT  
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA  
 CCAAGAGCCCCCAAGTGCACCTTCCCTAAGGTCCCTCCAGTGCTTGAATATCAGCGTGCTAAGT  
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA  
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC  
 TGCAGGGACTCGTGTCTTGGGGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTAC  
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTTGAGTCAT  
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG  
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCT  
 CCTGGACTCAGGGTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGG  
 GAACAATTTCCAAAACCTGTCCAGGGCGGGGGTTCGCTCTCAATCTCCCTGGGGCACTTTTCAT  
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA  
 CTGAGAAGTGGAAAAAAAAAA

MATARPPWMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDD  
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS  
PVYESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRRIPTKDVRPINVSSHCP SAGTKCL  
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGR DSCQGD SGGP  
VVCNGSLQGLVSWG DYPCARP NRPGVYT NLCKFTKWIQETIQANS

**FIGURE 227**

**ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCCAACTTGAGGACCGGCCGCGCGA**  
 CAAGCCGACGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGGCCCTGGCTGTGC  
 TGCTGGCTGTAGCTGTACCGGTGCCGTGCTCTTCTGAACCACGCCCACGCGCCGGGCACG  
 GCGCCCCACCTGTCTGTCAGCACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTCACTGTGGA  
 AAGGGCGGACAGCTCGCACCTCAGCATCCTCATTGACCCGCGCTGCCCCGACCTCACCGACA  
 GCTTCGCACGCCTGGAGAGCGCCAGGCCCTCGGTGCTGCAGGCGCTGACAGAGCACCAGGCC  
 CAGCCACGGCTGGTGGGCGACCAGGAGCAGGAGCTGCTGGACACGCTGGCCGACCAGCTGCC  
 CCGGTGCTGGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG  
 GCACGCTGGGGCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGCCGCCTCATCCAGCTTCTC  
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTACGCGACATCCTGGATGCCCT  
 GCAGAGGGACCGGGGGCTGGGCCGGCCCCGCAACAAGGCCGACCTTCAGAGAGCGCCTGCCC  
 GGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCGGCCCGGAGACTGTCTGGACGTCCTC  
 CTAAGCGGACAGCAGGACGATGGCGTCTACTGTCTTTCCACCCACTACCCGGCCGGCTT  
 CCAGGTGTACTGTGACATGCGCACGGACGGCGGGCTGGACGGTGTTCAGCGCCGGGAGG  
 ACGGCTCCGTGAACCTTCTTCCGGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTCACC  
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGAGCT  
 GCACGTGGACCTGGAGGACTTTGAGAATGGCACGGCCTATGCCGCTACGGGAGCTTCGGCG  
 TGGGCTTGTCTCCGTGGACCCTGAGGAAGACGGGTACCCGCTCACCCTGGCTGACTATTCC  
 GGCACCTGCAGGCGACTCCCTCCTGAAGCACAGCGGCATGAGGTTACCAACCAAGGACCGTGA  
 CAGCGACCATTAGAGAACAACCTGTGCCGCTTCTACCGCGGTGCCTGGTGGTACCGCAACT  
 GCCACACGTCCAACCTCAATGGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGC  
 GTGGAGTGGTCTCTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG  
 GCCGGTCCGGGAGGACCGCT**TAGACT**GGTGCACCTTGTCTTGGCCCTGGCTGGTCCCTGTCTGC  
 CCCATCCCCGACCCACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCCTGGCGGAC  
 CCACTCTCCAGTAGGGAGGGGCCGGGCCATCCCTGACACGAAGCTCCCTGGGCCGGTGAAGT  
 CACACATCGCCTTCTCGCCGTCCCCACCCCTCCATTTGGCAGCTCACTGATCTCTTGCCCTC  
 TGCTGATGGGGGCTGGCAAACCTTGACGACCCCAACTCCTGCCTGCCCCACTGTGACTCCGG  
 TGCTGTTTGGCGTCCCCTGGCCAGGATGTTGGAGTCTGCCCCAGGCACCTCTGCCCTGCCC  
 GGCCAAATACCCGGCATTATGGGGACAGAGAGCAGGGGGCAGACAGCACCCCTGGAGTCTC  
 CTAGCAGATCGTGGGGAATGTCAGGTCTCTCTGAGGTGAGGTCTGAGGCCAGTATCCTCCAG  
 CCCTCCCAATGCCAACCCCAACCCCGTTTCCCTGGTGCCAGAGAACCCACCTCTCCCCCAA  
 GGGCCTCAGCCTGGCTGTGGGCTGGGTGGCCCCATCCTACCAGGCCCTGAGGTGAGGATGGG  
 GAGCTGCTGCCTTTGGGGACCCACGCTCCAAGGCTGAGACCAGTTCCCTGGAGGCCACCCAC  
 CCTGTGCCCCGGCAGGCCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCACCTGCTCTCTG  
 TCTCAAATGAGGCCCAACCCATCCCCACCCAGCTCCCGGCCGTCTCTACCTGGGGCAGC  
 CGGGGCTGCCATCCCATTTCTCCTGCCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT  
 GGACTGCGCTAATGGGAAGCTCTTGGTCTTCTGGGCTGGGGCCTAGGCAGGGCTGGGATGAG  
 GCTTGTACAACCCCAACCAATTTCCAGGGACTCCAGGGTCTGAGGCCTCCAGGAGG  
 GCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCCATGAGGAGGCCAACCCCTGCC  
 ATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGGCCGAGTGGTCAAGGGACAGGGA  
 CCACCTCACCGGGCAAATGGGGTCCGGGGGACTGGGGCACCAGACCAGGCACCACTGGACA  
 CTTTCTTGTGTAATCCTCCCAACACCCAGCACGCTGTCTATCCCCACTCCTTGTGTGCACACA  
 TGCAGAGGTGAGACCCGCAGGCTCCAGGACCAGCAGCCACAAGGGCAGGGCTGGAGCCGGG  
 TCCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGCGTGCCTTACGTGAGGCCAGATGCAGGG  
 CGGCTTTTCCAAGGCCTCCTGATGGGGGCTCCGAAAGGGCTGGAGTCAGCCTTGGGGAGCT  
 GCCTAGCAGCCTCTCCTCGGGCAGGAGGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA  
 GGTGCCTAGGGGGTGTGGGGTTCGTTCTCCCTTCCCCTCCCACTGAAGTTTGTGCTTAAAA  
 AACAATAAATTTGACTTGGCACCACTGGGGGTGGTGGGAGAGGCCGTGTGACCTGGCTCTC  
 TGTCCAGTGCCACCAGGTATCCACATGCGCAG

**FIGURE 228**

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT  
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA  
QPRLVGDQEQELDLADQLPRLRARASELQTECMGLRKHGTLGQGLSALQSEQGRLIQLL  
SESQGHMAHLVNSVSDIILDALQDRGLGRPRNKADLQAPARGTRPRGCATGSRPRDCLDVL  
LSGQQDDGVYSVFPTHYPAGEQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT  
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAARYGSFGVGLFSVDPEEDGYPLTVADYS  
GTAGDSLLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG  
VEWSSWTGWQYSLKFSEMKIRPVREDR

**FIGURE 229**

GCAGTCAGAGACTTCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCCT  
 TGCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCT  
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG  
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC  
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC  
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACC  
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC  
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC  
 TGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG  
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG  
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAAACAAGAAGA  
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT  
 TGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG  
 TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG  
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA  
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC  
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT  
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG  
 TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA  
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTG  
 GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCAT  
 GTCTTCCTTACACTTGGTGGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC  
 ATCCTTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC  
 AGCAAATACACAAGGAATTCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT  
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG  
 AATCTCAAATCTCAATGCCTTATAAGCATTCTTCCTGTGTCCATTAAGACTCTGATAATTG  
 TCTCCCCTCCATAGGAATTTCTCCCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAG  
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA  
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAG  
 GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

MQAKYSSTRDMLDDGDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVL  
LIGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKL  
CRELYNKAGAHRCSPCTEQWKWHGDNQYQFYKDSKSWEDCKYFCLSENSTMLKINKQED  
LEFAASQSYSEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTS  
PRSRDCVAILNGMIFSKDCKELKRCVCERRAGMVKPESLHVPPETLGEGD

**FIGURE 231**

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG  
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG  
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG  
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA  
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA  
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT  
GTGGCTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA  
AGTNTCCTCATNTACTATACACACACCACTTCCC

**FIGURE 232**

GCCGAGCGCAAGAACCCTGCGCAGCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC  
 CGGGGATTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCCCGCGGGG  
 CCCGAGCCCTCCGGATCCGCCCCCTCCCCGGTCCCGCCCCCTCGGAGACTCCTCTGGCTGCT  
 CTGGGGGTTTCGCCGGGGCCGGGGACCCGCGGTCCGGGCGCC**ATG**CGGGGCATCGCTGCTGCTG  
 TCGGTGCTGCGGCCCCGAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTCACCCTGAGCCT  
 GCTCAGCGTCACCTGGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCCAACCTGGAGACTCTG  
 AGCTGCCGCCGCGCGGCAACACCAACGCGGCGCGCCGGCCCAACTCGGTGCAGCCCGGAGCG  
 GAGCGCGAGAAGCCCCGGGGCCGGCGAAGGCGCCGGGGAGAATTGGGAGCCGCGCGTCTTGCC  
 CTACCACCCTGCACAGCCCCGGCCAGGCCGCCAAAAAGGCCGTGAGGACCCGCTACATCAGCA  
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGCGGCTGCTGACCTCTCAGACCACGCTGCCC  
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTTCTTGAC  
 GGGCGCACGGGGCCGCGGGGCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC  
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGAGACTTTGAC  
 TGGTTCTTCTGTGTGCTGACACCACTACACGAGGCGCACGGCCTGGCACGCCTAACTGG  
 CCACCTCAGCCTGGCCTCCGCGGCCACCTGTACTTGGGCGGGCCCCAGGACTTCATCGGCG  
 GAGAGCCCCACCCCGGGCCGCTACTGCCACGGAGGCTTTGGGGTGCTGCTGTGCGCATGCTG  
 CTGCAACAACTGCGCCCCCACCTGGAAGGCTGCCGCAACGACATCGTCAGTGCGCGCCCTGA  
 CGAGTGGCTGGGTGCTGCTGCTGCTGATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGG  
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGACAGGAGGGGGACCCCTCAT  
 TTCCGAAGTGCCCTGACAGCCCACCTGTGCGTGACCCCTGTGCACATGTACCAGCTGCACAA  
 AGCTTTCGCCCCGAGCTGAACTGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGA  
 TCCAGAATAACCAGCCATCTGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCCGTGGGTATT  
 CCAGCACCATCCCGCCCCGGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA  
 GCACGCTTTCTCCTGCGCCGATGGCTCACCCCGCTGCCCACTGCGTGGGGCTGACCGGGCTG  
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCGGCCTTG  
 CGGCTCCAGAAGCAGCAGCTGGTGAAATGGCTACCGACGCTTTGATCCGGCCCCGGGGTATGGA  
 ATACACGCTGGACTTGACGCTGGAGGCACTGACCCCCAGGGAGGCGCCGGCCCCCTCACTC  
 GCCGAGTGACGCTGCTCCGGCCGCTGAGCCGCGTGAGATCTTGCCCTGTGCCCTATGTCACT  
 GAGGCCTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGG  
 CTTCTTGAGGGCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC  
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGCGCCATGCAGATGTCTTCGCACCT  
 GTCAAGGCCCCACGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGGTGCCATGGCTCAG  
 TGTGCAGACAGCCGCACCCTACCACTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCGC  
 TGGACACACTGTTCTGTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCCTGAACCGC  
 TGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCCAAGCCTTCCA  
 CCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCCGTGACACTGGCCGCT  
 TTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACTCCGACTACGTGGCAGCCCGTGGG  
 CGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT  
 GTTCTCTCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT  
 ACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGTACCACCGCTGCCTCCAGAGC  
 GTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG  
 CAACAGCACCT**TGA**CCCCACCCTGTCCCCGTGGGCCGTGGCATGGCCACACCCACCCCACTT  
 CTCCCCAAAACCAGAGCCACCTGCCAGCCTCGCTGGGCAGGGCTGGCCGTAGCCAGACCCC  
 AAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTGGGTCCCTGGGCTCTGGACAAGCACTGGG  
 GGACGTGGCCCCAGAGCCACCCACTTCTCATCCCAAACCCAGTTTCCCTGCCCCCTGACGCT  
 GCTGATTGCGGCTGTGGCCTCCACGTATTTATGCAGTACAGTCTGCCTGACGCCAGCCCTGC  
 CTCTGGGCCCTGGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAAGGAGGGAGCTGAGGAGGGG  
 GCATCTCCCAACTTCTCCCTTTTGACCCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA  
 AGTGTGAAAAA



**FIGURE 233**

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP  
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKKAVRTRYISTELGIRQRLLVAVL  
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE  
QHGDDEFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG  
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHYSHLELSPGEP  
VQEGDPHFRSALTAPVRDPVHMYQLHKAFARAELETTYQEIQELQWEIQNTSHLAVDGDRA  
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN  
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGRRPLTRRVQLLRPLSRVEI  
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA  
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL  
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGPGPPELGRDTGRFDRQAASEACFYNS  
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL  
YHRCLQSVLEGLGSRTQLAMLLFEQEQQNST

**FIGURE 234**

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT  
TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGAGAAAAGGAGT  
AGCTATTAGCCAATTCGGCAGGGCCCCGCTTTTTAGAACTTGATTTCCCTTTGAAGATGAAAG  
ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA  
CTGTATCCACCCAAATGTCACCGATTTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA  
GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG  
AGGGTTGCTCAACGCCCCGCCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG  
GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT  
TTCCCCGCCCTGAGACCTGCAGACCATCTGT**CATG**GCGGCTGGGCTGTTTGGTTTGAGC  
GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCCGCTCCGCTGGGA  
ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGGCCCCCAGAAC  
CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGTATGAGAAGAACCCA  
GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGTCTGGAACATGCGACTTGTCTTCTT  
CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA  
GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC  
CTTCCCATCATGGAATCCAACCTGCTTCGACCCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**  
**A**CCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC  
CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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**FIGURE 235**

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE  
DENLYEKNPDSHGYDKDFVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER  
LVKYREANGLPIMESNCFDPSKIQLPEDE

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GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC  
TCCCGGCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT  
GTGGCGGGAAAGCGGCCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA  
CGAAAACCTTGATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCGTTTTGGACG  
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC  
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT  
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAC TGCTTCGACCCCAGCA  
AGATCCAG

**FIGURE 237**

GCGGCGGGCT**ATG**CCGCTTGCTCTGCTCGTCCTGTTGCTCCTGGGGCCCCGGCGGCTGGTGCCT  
TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTTGTCATCACCCCGCTGCCTTCCGGGG  
ACGTAGCCGCCACATTCCAGTTCGCGACGCGCTGGGATTTCGGAGCTTCAGCGGGAAGGAGTG  
TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA  
GCTGCACCTGTCAATCACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCTTCCTGC  
AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCGAAGACACTGTCACTGATGTGGATAAA  
TCTTGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA  
CTCCACCAACACAGTCACTCCCCTGCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG  
ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC  
CCCTGGAAGAAGCTCTTGCCCTGTAGTTCGAAGGCAGGCCTCTCTGTGCTGCTGAAGGCAGA  
TCGCTTGTTCCACACCAGCTACCACTCCCAGGCAGTGCATATCCGCCCTGTTTGAGAAATG  
CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAGTTGTATTTGATGCCTTC  
ATCACGGGGCAGGGAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA  
GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACAACCAGGACA  
ACGAGACATTAGAGGTGCACCCACCCCCGACCACTACATATCAGGACGTCATCCTAGGCACT  
CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT  
CAACATCCAGCTCAAGTGGAAGAGACCCCCAGAGAATGAGGCCCCCCCCAGTGCCCTTCCTGC  
ATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC  
AACACCCACCCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG  
GCTGTATGTGCACACCCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC  
ACTACCAGCCTGCCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTGAGCTGCCG  
GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA  
CACGCCAGATCCTAACCATGGCTTCTATGTCAGCCCATCTGTCTCAGCGCCCTTGTGCCCA  
GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCCTCTTCAACAGCCTGTTCCCA  
GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC  
GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT  
GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT  
GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACTCT**TGA**ATT  
CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT  
TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTGAGGGC  
CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGTAATTTGAATTAA  
CTTAGAAATTCATTTCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA  
AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACACAGAAAGGTC  
GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGA  
TGGAGTTTACTGTTTGTGGAATAAAAACGGCTGTTTCCGTGGAAAAA

**FIGURE 238**

MPLALLVLLLLGPGGWCLAEP PRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY  
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDKSWK  
ELSNVLSGIFCASLNFIDSTNTVTPTASF KPLGLANDTDHYFLRYAVLPREVVCTENLTPWK  
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSSISWELRQTL SVVFDAFITG  
QGKDWLSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT  
YAIYDLLDTAMINNSRNLNIQLKWKRPPE NEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH  
PYRAFPVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS  
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD  
GSNYFVRLYTEPLL VNLPTPDFSMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA  
KRLANLIRRARGVPPL

**FIGURE 239**

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG  
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCCAGCTGACAACGTACGC  
TGCTTCAAGTCCGATCCTCCCCAGTGT CACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG  
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA  
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC  
TCCTCCTCTACCAGGTGTCCTCAGAAATGAATGCTGGGTCCTTTCTACCTCTGGGGGTCACTC  
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC  
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG  
TCCAGACCCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT  
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC  
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCCTCACCAGATG  
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCCAGCCTCTAGAACTGTAAGAAATAAATAT  
TTGCTGTTTATAATCCAA

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**FIGURE 240**

MGSSSFVLVMVSLVLTSLVAVEGVKEGIEKAGVCPADNVRCEKSDPPQCHTDQDCLGERKCC  
YLHCGFKCVIPVKELEEKGKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

**Signal sequence:**

amino acids 1-19

**N-myristoylation sites:**

amino acids 23-29, 27-33, 32-38, 102-108

**WAP-type 'four-disulfide core' domain signature:**

amino acids 49-63

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**FIGURE 241**

AACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGG  
 AACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC  
 TCTAGAACCCGACCCACCACC**ATG**AGGTCTGCTGTGGAGATGCAGGCACCTGAGCCAAGG  
 CGTCCAGTGGTCCTTGCTTCTGGCTGTCTGGTCTTCTTTCTCTTCGCCTTGCCCTCTTTTA  
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT  
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA  
 TGCAGAGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA  
 CCGGAGACAGAGGAAAGGAGGCCAACCCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC  
 ACAGCACAGAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC  
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC  
 AGGACACAAAGACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG  
 GTGTCAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTCCCAAAGTCA  
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA  
 CAGCAGTCATCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCCCTTTCCAG  
 AGCCCCACGACGCAGAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG  
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTG  
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCAACCTCACTCTC  
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACC  
 CTTTGGCTTCATGGAGCTCACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG  
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGT  
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCA  
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC  
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT  
 CGGGGTTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACTTCCTGGAAGGCAC  
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT  
 TCTGGTTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG  
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGA  
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC  
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT  
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA  
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCCTGGTC  
 CCGGAAGTGCCAAAGCCAAGAAG**TGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC  
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA  
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT  
 GGCAAATGGCTAATTGAGGTTCTGAAGTTCTTCAGTACATTGCTGTAGGTCTGAGGCCAGG  
 GATTTTTAATTAAATGGGGTGATGGGTGGCCAATACCACAATTCCTGCTGAAAAACACTCTT  
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTTACAGAAACATATAGATCTG  
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACCTCACTAC  
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGGTCTATACTTGTCCTTG  
 TCTTTAAGCTATTTGACAACCTCTACGTGTTGTAGAAAAGTGAATAATAACAAATGATTGTT  
 GTCCATGGAAAGGCAAATAAATTTTCTACAGTGAAAAAAAAAAAAAAAA

**FIGURE 242**

MRSC LWRCRHLSQGVQWSLLLAVLVFFLEFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP  
KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW  
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGGQTRKLTASRTVSEKHQG  
KAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPKEKKPQATPPPAPFQSPTTQRN  
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHF  
NQSEWDRLEHFAPPFGEFMEFNYSLVQKVVTREPPVPQQQLLLASLPAGSLRCITCAVVGNGG  
ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLLILGNRGFKNVP  
LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLHPDFL  
RYMKNRFLRSKTLGDGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW  
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRP GPGTAKAKN

**Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Lumenal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

**FIGURE 243**

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG  
GAGCAGCGAGTGGAAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT  
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA  
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT  
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC  
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG  
ACAAGAGATTTATTTTTGCAGACAGACTCTTCCATAAGTCCTTTGAGTTTGTATGTTGTTG  
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACCTATTT

**FIGURE 244**

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPPLYFSPKCSKH FHRLYHNT  
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

09963-11604  
"T.T.T." 89/650



**FIGURE 246**

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC  
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILEVAVVATTICCFLCSCCYLYRRRQQQLQSP  
FEGQEIPMTGIPVQPVPYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP  
YMPPQPSYPGA

**Transmembrane Domains:**

amino acids 10-28, 85-110

**N-glycosylation Site:**

amino acids 38-41

**N-myristoylation Sites:**

amino acids 5-10, 88-93

**FIGURE 247**

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGGCGGCAAGGGTGAGGGCGGCCCCAGAA  
 CCCCAGGTAGGTAGAGCAAGAAG**ATG**GGTGTCTTCTGCCCCCTCAAATGGTCCCTTGCAACCATG  
 TCATTTCTACTTTCCTCACTGTTGGCTCTCTTAACCTGTGTCCACTCCTTCATGGTGTAGAG  
 CACTGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCTTGGGAATAAAATACGACTTC  
 CTGAGTACGTATCCAGTTTCAATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACC  
 TTCTGGGGAACACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAGCACCATCATCCTGCA  
 TAGTCACCACCTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG  
 AAGAACCCTGCAGGTCCTGGAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCGAG  
 CCCCTCCTTGTCGGGCTCCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTTCGGAGAC  
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAACTGAGGATACTAGCAT  
 CAACACAATTTGAACCCACTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC  
 AAAGCAAGTTTCTCAATCAAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCCAATATGCC  
 ATTGGTGAAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGA  
 AGATGAGCACCTATCTGGTGGCCTTCATCATTTTCAAGATTTTGAGTCTGTGCAAGATAACC  
 AAGAGTGGAGTCAAGGTTTCTGTTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGC  
 ACTGGATGCTGCGGTGACTCTTCTAGAATTTTATGAGGATTATTTTCAAGCATACCGTATCCCC  
 TACCCAAACAAGATCTTGCTGCTATTTCCCGACTTTTCACTGCTGGTGTATGGAAAACCTGGGA  
 CTGACAACATATAGAGAATCTGCTCTGTTGTTTATGTCAGAAAAGTCTTCTGCATCAAGTAA  
 GCTTGGCATCACAGTGAAGTGTGGCCCATGAACCTGGCCACCAGTGGTTTGGGAACCTGGTCA  
 CTATGGAATGGTGAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTG  
 TCTGTCACTGTGACCCATCCTGAAGTGAAGTTGGAGATTATTTCTTTGGCAAATGTTTTGA  
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCCTGTGTCTACACCTGTGGAAAATCCTG  
 CTCAGATCCGGGAGATGTTTGATGATGTTTCTTATGATAAGGGAGCTTGATTTCTGAATATG  
 CTAAGGGAGTATCTTAGCGCTGACGCATTTTAAAGTGGTATTGTACAGTATCTCCAGAAGCA  
 TAGCTATAAAAATACAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAG  
 ATGGTGTAAAAGGGATGGATGGCTTTTGCTCTAGAAGTCAACATTCATCTTCATCCTCACAT  
 TGGCATCAGGAAGGGGTGGATGTGAAAACCATGATGAACACTTGGACACTGCAGAGGGGTTT  
 TCCCCTAATAACCATCACAGTGAAGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA  
 AGGGCTCTGACGGCGCCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTCATCACC  
 AGCAAATCCAACATGGTCCATCGATTTTTTGCTAAAAACAAAAACAGATGTGCTCATCCTCCC  
 AGAAGAGGTGGAATGGATCAAATTTAATGTGGGCATGAATGGCTATTACATTGTGCATTACG  
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAAGGAACACACACAGCAGTCAGCAGT  
 AATGATCGGGCAAGTCTCATTAAACAATGCATTTTCACTCGTCAGCATTGGGAAGCTGTCCAT  
 TGAAAAGGCCCTTGGATTTATCCCTGTACTTGAAACATGAACTGAAATTATGCCCGTGTTC  
 AAGGTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG  
 GAAACTCAATTCAGGCCTTCCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG  
 GACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCGGAGTGAACACTACTCCTCGCCTGTG  
 TGCACAACATATCAGCCGTGCGTACAGAGGGCAGAAGGCTATTTAGAAAAGTGGAAGGAATCC  
 AATGGAACTTGAGCCTGCCTGTGACGCTGACCTTGGCAGTGTGTGCTGTGGGGGCCAGAG  
 CACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTTTTCTTTGTCCAGTACTGAGAAAA  
 GCCAAATTGAATTTGCCCTCTGCAGAACCCAAAATAAGGAAAAGCTTCAATGGCTACTAGAT  
 GAAAGCTTTAAGGGAGATAAAAATAAAAACTCAGGAGTTTCCACAAATCTTACACTCATTGG  
 CAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAGGAAAAACTGGAACAAACTTG  
 TACAAAAGTTTGAACCTGGCTCATCTTCCATAGCCACATGGTAATGGGTACAACAAATCAA  
 TTCTCCACAAGAACACGGCTTGAAGAGGTAAAAGGATTTCTCAGCTCTTTGAAAGAAAATGG  
 TTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATTGAAGAAAACATCGGTTGGATGG  
 ATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAAAGCTTGAACGTATG**TAAAAA**  
 TTCTCCTTGGCCGGTTCTGTTATCTCTAATCACCAACATTTTGTGTGAGTGTATTTTCAA  
 ACTAGAGATGGCTGTTTTGGCTCCAACCTGGAGATACTTTTTTCCCTTCAACTCATTTTTTGA  
 CTATCCCTGTGAAAAGAATAGCTGTAGTTTTTTCATGAATGGGCTTTTTTCATGAATGGGCTA  
 TCGCTACCATGTGTTTTGTTTCATCACAGGTGTTGCCCTGCAACGTAAACCCCAAGTGTGGGT  
 TCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 248**

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH  
 YDLLIHANLTTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLE  
 HPPQEQIALLAPEPLLVLGPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA  
 ARMAFPFCFDEPAFKASF SIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA  
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAVTLLEFYEDYFSIPYPLPKQDLAA  
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELHQWFGNLVTMEWWNDL  
 WLNEGFAKFMFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD  
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGM DG  
 FCSRSQHSSSSSSHHWQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD  
 TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL  
 TGLLKGHTAVSSNDRASLINNAFQLV SIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP  
 MYKLM EK RDMNEVETQFKAFLIRLLRDLIDKQ TWTDEGSVSEQMLRSELLLLACVHNYQPCV  
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALC  
 RTQNKEKLQWLLDESFKGDKIKTQEF PQILT LIGRNPVGYPLAWQFLRKNWNKLVQKFELGS  
 SSIAHVMVGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQT IETIEENIGWMDKNFDKIR  
 VWLQSEKLERM

**Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360



**FIGURE 249**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC  
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC  
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG  
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT  
 GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA  
 ACTGCAATAGGAAAGATTTTCTGACCTGTTCATCGGGGGACCACCATTTATGACACACGGAAAC  
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG  
 GCTGCAGCACTGTTGGGGCTCAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTC  
 CTACCTGTGTGCAGCCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
 GCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT  
 GAGCATTACAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG  
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
 GTGGGGAGTGGTTTGCCCTTCCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA  
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC  
 CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCA  
 AACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

**FIGURE 250**

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPRQWTPKNTSCDSGLGCQDTLMLI  
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMPPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSENTEMCEVGQVCQETL  
LLIDVGLTSTLVGKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVC  
PSC

**FIGURE 251**

CGGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT  
CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG  
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG  
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCG  
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCGT CAT  
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC  
TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG  
AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC  
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA  
CGCCCAGCTGTCCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCA  
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCCGTGTCTTCATCGGCATCAAC  
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA  
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT  
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG  
GAGAACATG**TGAG**CCCTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCAGGGTT  
GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG  
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG  
AAAGTGTTCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA  
ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC  
TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

MRGNLALVGVLI SLAFLSLLPSGHQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG  
PTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE  
MDNQVSQLTSELKF IKNVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN  
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS  
GGWNDVACHTTMYFMCEFDKENM

|  | 1970  | 1980  | 1990  | 2000  | 2006  |
|--|-------|-------|-------|-------|-------|
| GDP per capita (US\$)                              | 1,000 | 1,500 | 2,000 | 2,500 | 2,800 |
| Population (millions)                              | 100   | 110   | 120   | 130   | 140   |
| Total GDP (US\$ billion)                           | 100   | 165   | 240   | 325   | 400   |
| Government expenditure (% of GDP)                  | 15    | 18    | 20    | 22    | 25    |
| Private consumption (% of GDP)                     | 60    | 62    | 64    | 66    | 68    |
| Investment (% of GDP)                              | 25    | 20    | 16    | 12    | 7     |
| Exports (% of GDP)                                 | 10    | 12    | 14    | 16    | 18    |
| Imports (% of GDP)                                 | 8     | 10    | 12    | 14    | 16    |
| Current account balance (% of GDP)                 | -2    | -2    | -2    | -2    | -2    |
| Public debt (% of GDP)                             | 5     | 10    | 15    | 20    | 25    |
| Foreign direct investment (% of GDP)               | 0     | 0     | 0     | 0     | 0     |
| Official development assistance (% of GDP)         | 0     | 0     | 0     | 0     | 0     |
| Net international reserves (% of GDP)              | 0     | 0     | 0     | 0     | 0     |
| Unemployment rate (%)                              | 5     | 5     | 5     | 5     | 5     |
| Inflation rate (%)                                 | 5     | 5     | 5     | 5     | 5     |
| Interest rate (%)                                  | 5     | 5     | 5     | 5     | 5     |
| Exchange rate (US\$/local unit)                    | 1     | 1     | 1     | 1     | 1     |
| Life expectancy at birth (years)                   | 50    | 55    | 60    | 65    | 70    |
| Fertility rate (children/woman)                    | 5     | 4     | 3     | 2     | 1     |
| Urban population (% of total)                      | 20    | 30    | 40    | 50    | 60    |
| Rural population (% of total)                      | 80    | 70    | 60    | 50    | 40    |
| Population growth rate (%)                         | 2     | 2     | 2     | 2     | 2     |
| Mortality rate (per 1,000 live births)             | 20    | 15    | 10    | 5     | 2     |
| Infant mortality rate (per 1,000 live births)      | 100   | 80    | 60    | 40    | 20    |
| Maternal mortality ratio (per 100,000 live births) | 500   | 400   | 300   | 200   | 100   |
| Adult literacy rate (%)                            | 10    | 20    | 30    | 40    | 50    |
| Primary school enrollment rate (%)                 | 50    | 60    | 70    | 80    | 90    |
| Secondary school enrollment rate (%)               | 20    | 30    | 40    | 50    | 60    |
| Tertiary school enrollment rate (%)                | 5     | 10    | 15    | 20    | 25    |
| Research and development expenditure (% of GDP)    | 0     | 0     | 0     | 0     | 0     |
| Health expenditure (% of GDP)                      | 5     | 6     | 7     | 8     | 9     |
| Social security expenditure (% of GDP)             | 0     | 0     | 0     | 0     | 0     |
| Environmental protection expenditure (% of GDP)    | 0     | 0     | 0     | 0     | 0     |
| Disaster relief expenditure (% of GDP)             | 0     | 0     | 0     | 0     | 0     |
| Other social services expenditure (% of GDP)       | 0     | 0     | 0     | 0     | 0     |
| Capital formation (% of GDP)                       | 25    | 20    | 16    | 12    | 7     |
| Fixed capital formation (% of GDP)                 | 20    | 18    | 15    | 12    | 7     |
| Consumption of fixed capital (% of GDP)            | 5     | 2     | 1     | 1     | 1     |
| Government revenue (% of GDP)                      | 15    | 18    | 20    | 22    | 25    |
| Government expenditure (% of GDP)                  | 15    | 18    | 20    | 22    | 25    |
| Balance of payments (% of GDP)                     | 0     | 0     | 0     | 0     | 0     |
| Trade balance (% of GDP)                           | 2     | 2     | 2     | 2     | 2     |
| Services balance (% of GDP)                        | 0     | 0     | 0     | 0     | 0     |
| Income balance (% of GDP)                          | 0     | 0     | 0     | 0     | 0     |
| Current transfers balance (% of GDP)               | 0     | 0     | 0     | 0     | 0     |
| Capital transfers balance (% of GDP)               | 0     | 0     | 0     | 0     | 0     |
| Financial account balance (% of GDP)               | 0     | 0     | 0     | 0     | 0     |
| Direct investment balance (% of GDP)               | 0     | 0     | 0     | 0     | 0     |
| Portfolio investment balance (% of GDP)            | 0     | 0     | 0     | 0     | 0     |
| Reserve assets balance (% of GDP)                  | 0     | 0     | 0     | 0     | 0     |
| Other financial account balance (% of GDP)         | 0     | 0     | 0     | 0     | 0     |
| Net international reserves (% of GDP)              | 0     | 0     | 0     | 0     | 0     |
| Debt service (% of GDP)                            | 0     | 0     | 0     | 0     | 0     |
| Debt repayment (% of GDP)                          | 0     | 0     | 0     | 0     | 0     |
| Debt interest (% of GDP)                           | 0     | 0     | 0     | 0     | 0     |
| Debt forgiveness (% of GDP)                        | 0     | 0     | 0     | 0     | 0     |
| Debt restructuring (% of GDP)                      | 0     | 0     | 0     | 0     | 0     |
| Debt cancellation (% of GDP)                       | 0     | 0     | 0     | 0     | 0     |
| Debt conversion (% of GDP)                         | 0     | 0     | 0     | 0     | 0     |
| Debt reduction (% of GDP)                          | 0     | 0     | 0     | 0     | 0     |
| Debt increase (% of GDP)                           | 0     | 0     | 0     | 0     | 0     |
| Debt stability (% of GDP)                          | 0     | 0     | 0     | 0     | 0     |
| Debt sustainability (% of GDP)                     | 0     | 0     | 0     | 0     | 0     |
| Debt risk (% of GDP)                               | 0     | 0     | 0     | 0     | 0     |
| Debt management (% of GDP)                         | 0     | 0     | 0     | 0     | 0     |
| Debt policy (% of GDP)                             | 0     | 0     | 0     | 0     | 0     |
| Debt strategy (% of GDP)                           | 0     | 0     | 0     | 0     | 0     |
| Debt framework (% of GDP)                          | 0     | 0     | 0     | 0     | 0     |
| Debt instrument (% of GDP)                         | 0     | 0     | 0     | 0     | 0     |
| Debt maturity (% of GDP)                           | 0     | 0     | 0     | 0     | 0     |
| Debt currency (% of GDP)                           | 0     | 0     | 0     | 0     | 0     |
| Debt sector (% of GDP)                             | 0     | 0     | 0     | 0     | 0     |
| Debt type (% of GDP)                               | 0     | 0     | 0     | 0     | 0     |
| Debt category (% of GDP)                           | 0     | 0     | 0     | 0     | 0     |
| Debt class (% of GDP)                              | 0     | 0     | 0     | 0     | 0     |
| Debt group (% of GDP)                              | 0     | 0     | 0     | 0     | 0     |
| Debt family (% of GDP)                             | 0     | 0     | 0     | 0     | 0     |
| Debt lineage (% of GDP)                            | 0     | 0     | 0     | 0     | 0     |
| Debt ancestry (% of GDP)                           | 0     | 0     | 0     | 0     | 0     |
| Debt descent (% of GDP)                            | 0     | 0     | 0     | 0     | 0     |
| Debt origin (% of GDP)                             | 0     | 0     | 0     | 0     | 0     |
| Debt source (% of GDP)                             | 0     | 0     | 0     | 0     | 0     |
| Debt root (% of GDP)                               | 0     | 0     | 0     | 0</   |       |

**FIGURE 253**

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG  
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC  
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT  
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG  
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC  
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA  
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA  
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCC  
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC  
TTTATAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT  
ATCCCCGAGAGCAGAATAGGTACTCCACTTCGGGACTCCTGGACTGCATTAGGAAGACCTC  
TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGT  
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA  
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT  
CCTACATTAAAAATATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA  
AA

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## **FIGURE 254**

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK  
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLLPSVRVPRPLHPNQLGSTGK  
SSLGTEEQRPL

### **Important features:**

#### **Signal peptide:**

amino acids 1-18

#### **Tyrosine kinase phosphorylation site.**

amino acids 36-45

#### **N-myristoylation site.**

amino acids 33-39, 59-65

#### **Amidation site.**

amino acids 90-94

#### **Leucine zipper pattern.**

amino acids 43-65

#### **Tachykinin family signature.**

amino acids 86-92

05997683-11101



**FIGURE 256**

MSCVLGGV I PLG L L F L V C G S Q G Y L L P N V T L L E E L L S K Y Q H N E S H S R V R R A I P R E D K E E I L M L  
H N K L R G Q V Q P Q A S N M E Y M V S A G S G R R G W H R G W G L G H Q P A L F P S Q L C S P A S A C D G W L R V S S G R  
G G S R L C S V L F V C F E T G S H S A T D A G V Q W H N R H A L K P

### Important features:

**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89



**FIGURE 257**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATGGG**  
GTCTGGGCTGCCCCCTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG  
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC  
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC  
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG  
TGTCTTCTTGGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT  
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTCTGGTATGCTG

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**FIGURE 258**

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFELLEKLCLLLHLPSTGTS  
VTLHHARSQHHVVCNT

05997633 414604

**FIGURE 259**

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT  
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAAACAATTAACTGTTAGGATTGCAGT  
**TATG**ATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC  
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTTGAAAATGAATGCTTAGTGGATCTG  
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCCCTCC  
CTCCGATTGTTCTAAA**TAA**TTGAAAGATGTCTGCTGTGGAAAAGGCATGTATTTAAATCTG  
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTT  
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA  
GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT  
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT  
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC  
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA  
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGA  
ATAAAAGTTCATATCTACCC

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## **FIGURE 260**

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECCLVDLCLLRICYKLSGVPNQCRVPLP  
SDCSK

**Important features:**

**Signal peptide:**

amino acids 1-29

09997693-11304

**FIGURE 261**

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT  
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTGTTTGCAGGATGATGGTGGCCCTT  
 CGAGGAGCTTCTGCATTGCTGGTCTGTTTCTTGCAGCTTTTCTGCCCCGCGCAGTGTAC  
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGAGCAAGGGCTGG  
 AAAAATGTACCCAAGCAACGAGGGCATAACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA  
 TCTGTCATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACCTT  
 GGCCTGAGAGTTGAACGTGCCCAACGGGAGATTGACTACATAACAATACCTTCGAGAGGCTG  
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA  
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC  
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA  
 ACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC  
 ATACGGGCATTATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTC  
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTTCATAACCAAGCAACTT  
 CTAATGAGATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA  
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT  
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCA  
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTATGGGATACCCCATGCAGAAGCCAG  
 GATGCTGAAGCCTCATTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA  
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC  
 CCAACTTGTTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT  
 AAGCAGCTCTATGCCTGGAATGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAAA  
 GCTGCCTCTGAAGTAAATGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT  
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG  
 AGTGTGTAGAAGTGGAATACGTATGCCTCCTTTCCCAATGTCAGTGCCTTAGGTATCTTC  
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAA  
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTTTTACT  
 GCTCCCCAGCATTTACTGTAACCTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC  
 CCCTAATATTACCACTGGCTTTTCTCTCCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTT  
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATACTATTAATATTTCTTT  
 CTTTTCTTTTCTTTTTTTTGGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTCC  
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC  
 CACACCTGGCTTAAAATACTATTTCTTATTGAGGTTTAACTCTATTTCCCCTAGCCCTGTC  
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAATATTAACATTTGAATATCGCTTT  
 CCAGGTGTGGAGTGTGTCACATCATTGAATTCTCGTTTACCTTTGTGAAACATGCACAAG  
 TCTTTACAGCTGTCAATTCTAGAGTTTAGGTGAGTAACACAATTACAAAGTGAAAGATACAGC  
 TAGAAAATACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAATACGTATGTT  
 TGTTTACCTACTCTTATAGTCAATGCGTTTCATCGTTTCAGCCTAAAAATAATAGTCTGTCCC  
 TTTAGCCAGTTTTTATGCTGTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATTCCTCC  
 AGAAAACCAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTTGTCTTGCTGTCTCTGT  
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

MMVALRGASALLVLFLLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE  
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL  
QEAEEEKKIRTLNLNASCDNMLMGIKSLKIVKKMMDTHGSMKDAVYNBPKVYLLIGSRNNTV  
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLEFFHNQATSNEIIKYNLQKRTVED  
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEIPGTLGVEHSWDT  
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPRSHSMIH  
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK



**FIGURE 264**

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK  
QYQRIRKEKPQQHNFTHRLLAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ  
REHRSMRANVELDHATLVRFSPDCRAFIWVLANGDTLRVFKMTKREDGGYTFTATPEDFPPK  
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASC  
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV  
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH  
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQRLQQQLTQ  
AQETLKSLGALKK

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

**Beta-transducin family Trp-Asp repeat protein.**

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308



**FIGURE 265**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG  
CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC  
TCCTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGT  
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT  
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA  
AGCACCACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC  
CGCTGCTCCATGGACTTGAAGAACATCAATTTTTTAGGCGCTTGCCTGGTCTCAGGATACCCA  
CCATCCTTTTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC  
TCTCCAGTCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG  
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG  
CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTG GTA  
AATGGCAGAAAGGACATTCCCCCTCCCCTCCCCAGGTGACCTGCTCTCTTTCCTGGGCCCTG  
CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTTGGGCACAGGCTCTTGGGT  
GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGG  
ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC  
TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA  
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA  
CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT  
TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAA  
TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCCTTTCCA  
AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG  
TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTAGACCAGGGAGG  
CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

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## **FIGURE 266**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHP  
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

059763-1164  
" 6392550

**FIGURE 267**

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGCTTTC  
CTCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC  
TGCTGCCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG  
CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA  
GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT  
CCTCTGTGCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG  
TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT  
TTCAAAGGAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT  
GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG  
GCTTCTCTGGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA  
GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT  
TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAATGAT  
TGTGTGAAACTGCCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGTATT  
GTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTA  
TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA  
CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA  
TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG  
TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC  
TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG  
GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA  
CACCCTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

**FIGURE 268**

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKAALEYLEDIDLKTLEKEPR  
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF  
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFILGGVFV  
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

**FIGURE 269**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCC  
GGCCAGGTGCCCCGTCGCAGGTGCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA  
AGCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTG  
CTTCTGGCGCTGGGCCTGCCGTTCCCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA  
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG  
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG  
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG  
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG  
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCC  
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG  
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG  
GCTATTCACCTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAA

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**FIGURE 270**

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV  
VFSLLAALLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

099733-1150  
P.O. Box 6394550

**FIGURE 271**

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGT  
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTG  
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT  
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC  
CTACCAAAGCTGTCAAACCCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA  
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG  
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA  
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT  
TTATTAATTTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA  
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCCTTACAGAATTGACATTTTAA  
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA  
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

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**FIGURE 272**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK  
GIVKGRNLDSRGLILGAEAWGRGVKKNT

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100



**FIGURE 273**

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTTATTTCAGAGGTTTTGTTTTCTCTTAGTTCT  
 GTGCCTGCTGCACCAGTCAAATACTTCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATA  
 TTGTCATTGTTATAGATCCTAGTGTGCCAGAAAGATGAAAAATAATTGAACAAATAGAGGAT  
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA  
 TGTATCTATATTAATTCCCTGAGAATTGGAAGGAAAATCCTCAGTACAAAAGGCCAAAACATG  
 AAAACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCA  
 TACACCAAGCAGTTCACAGAATGTGGAGAGAAAGGCCAATACATTCACCTCACCCCTGACCT  
 TCTACTTGAAAAAAACAAAATGAATATGGACCACCAGGCAAACCTGTTTGTCCATGAGTGGG  
 CTCACCTCCGGTGGGGAGTGTGGTATGAGTACAATGAAGATCAGCCTTTCTACCGTGCTAAG  
 TCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAA  
 GTGTCAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACGTGTATG  
 GAAAAGATTGTCAATTCTTTCTGATAAAGTACAACAGAAAAAGCATCCATAATGTTTATG  
 CAAAGTATTGATTCTGTTGTTGAATTTTGAACGAAAAAACCCATAATCAAGAAGCTCCAAG  
 CCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAATTCTGAGGATT  
 TTA AAAACACCATAACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTTGCTGAAGATC  
 AGTCAAAGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAGGACCGCT  
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGG  
 TGGGGATGGTTCATTTTGTATGACTGCCACTATTGTAATAAGCTAATCCAAATAAAAAGC  
 AGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAACTTCCAT  
 CTGCTCTGGAATTAATATGCATTTAGGTGATTGGAGAGCTACATTCCCAACTCGATGGAT  
 CCGAAGTACTGCTGCTGACTGATGGGGAGGATAAAGTCAAGTTCTTGTATTGATGAAGTG  
 AAACAAAGTGGGGCCATTGTTTCATTTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAT  
 AGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTTTCAGATGAAGCTCAGAACAATG  
 GCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAAAGTCCCTT  
 CAGCTCGAAAGTAAGGGATTAACTGAATAGTAATGCCTGGATGAACGACACTGTCTATAAT  
 TGATAGTACAGTGGGAAAGGACACGTTCTTTCTCATCACATGGAACAGTCTGCCTCCCAGTA  
 TTTCTCTCTGGGATCCCAGTGGAAACAATAATGGAAAATTTACAGTGGATGCAACTTCCAAA  
 ATGGCCTATCTCAGTATTTCCAGGAAGTGCAAAAGTGGGCACTTGGGCATACAATCTTCAAGC  
 CAAAGCGAACCAGAAACATTAAGTATTACAGTAAGTCTCGAGCAGCAAAATTTCTGTGTC  
 CTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCCAGCCCAATGATT  
 GTTTACGCAGAAATTTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTTAT  
 TGAATCACAGAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT  
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAATGGCAGATAT  
 AGCTTAAAAGTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTACGGCCTCCACT  
 GAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATTGAAGCAAACCCGCCAA  
 GACCTGAAATTGATGAGGATACTCAGACCACCTTGGAGGATTTTCAGCCGAACAGCATCCGGA  
 GGTGCATTTGTGGTATCACAAAGTCCCAAGCCTTCCCTTGCCGACCAATACCCACCAAGTCA  
 AATCACAGACCTTGATGCCACAGTTCATGAGGATAAGATTATTCTTACATGGACAGCACCAG  
 GAGATAATTTTGTATGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGAAGTATTCTT  
 GATCTAAGAGACAGTTTTTGTATGCTCTTCAAGTAAATACTACTGATCTGTCAACAAAGGA  
 GGCCAACTCCAAGGAAAGCTTTGCATTTAAACCAGAAAATATCTCAGAAGAAAATGCAACCC  
 ACATATTTATTGCCATTAAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATT  
 GCACAAGTAAGTTTGTATCCCTCAAGCAATCCTGATGACATTGATCCTACACCTACTCC  
 TACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTTCTACGCTGGTAT  
 TGTCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAAGTACCACCATT**TGA**ACCTTA  
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTTTAAAAACAAAACAAATGTAAGT  
 AAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAAACTCATAAAAAATAATT  
 TTAAGATGTCGAAAAGGATACTTTGATTAAATAAAAAACACTCATGGATATGTAAAAACTGT  
 CAAGATTAATAATTAAAGTTTCATTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAAC  
 AAAGATCCTTTTTCTACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTTCTGAAAT  
 GATATTTCAAATTGCATCAAGAAATTAATAATCATCTATCTGAGTAGTCAAAATACAAGTAAA  
 GGAGAGCAATAAACAAACATTTGGAAAAA  
 AA

**FIGURE 274**

MGLFRGFVFLLLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTASTY  
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC  
 GEKGEYIHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR  
 CSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE  
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLV  
 LDKSGSMGGKDRLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM  
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVH  
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT  
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG  
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQG  
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDBGVYSRYFTAYTENGRYSLKVRAGH  
 GANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLEDFSRTASGGAFVVSQV  
 PSLPLPDQYPPSQITDLDATVHEDKIIILTWAPGDNFDVGKVQRYIIRISASILDLRDSFDD  
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP  
 QANPDDIDPTPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

**FIGURE 275**

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATAACGTCCCCG  
 GGCAGGGGTGACAACAGGTGTCATCTTTTTGATCTCGTGTGTGGCTGCCTTCTATTTCAAGGAAAG  
 ACGCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACC  
 CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTT  
 GTGGTTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGA  
 GGGTGGACCAGAAGAAAGGAAAGGTCCCTCTTGTCTGTTGGCTGCACATCAGGAAGGCTGTGATGGG  
 AATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCTTTAAAA  
 GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATG  
 CAAGCAGCTCCGGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGG  
 GCCCCGGCTTTGAGGGATGCCACCGTTCTGGACGCATGGCTGATTCTGAATGATGATGGTTCGCC  
 GGGGCTGCTTGGCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGCTCCTCTGCTGTGCTATCTCTGT  
 CCTGTACATGTTGGCCTGCACCCCAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGGCCAACAGC  
 CCCACGGGGAAGGAGGGGTACCAGGCCGTCTTCAGGAGTGGGAGGAGCAGCACCGCAACTACGTGA  
 GCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGTGCAGGAGAGGAGTGCAGGAGAGGAGTCA  
 TGGCAGTACCAAGCCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAG  
 GCCGACCTCCTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGG  
 CCACAGAGTATGCAGCAGTGCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG  
 CTTTACCCGCCACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 GAATCAGCCTTGGAGACCTTGAACAATCCTGCAGAGAACAGCCCCAATCACCCTCCTTACACGGCCT  
 CTGATTTTATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGGACATTTGTATGAGCTCACCTTCAA  
 AGGGGACCACAAACACGAATTCAAACGGCTCATCTTATTTGACCATTCAGCCCCATCAAGAAAGTG  
 AAAATGAAAAGCTCAACATGGCCAAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGG  
 ACAAGTTCCGGCAGTTTATGCAGAATTTTCAAGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCT  
 CACTGTTGTTTACTTTGGGAAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAA  
 GCTGCCAACTTCAGGAACCTTACCTTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGGACTTG  
 ATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACGTCCTTCTCTTTTTCTGTGATGTGGACATCTACTT  
 CACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAGGTATTTTATCCAGTT  
 CTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAAACAGC  
 AGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTTGGATTGGGATGACGTGTCAATATCG  
 GTCAGACTTCATCAATATAGGTGGGTTTGTATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC  
 CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTCCACC  
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGAGCAGTACAAGATGTGCATGCAGTCCAA  
 GGCCATGAACGAGGCATCCCACGGCAGCTGGGCATGCTGGTGTTCAGGCACGAGATAGAGGCTCAC  
 CTTTCGCAAAACAGAAACAGAGCAAGTAGCAAAAAACATGAACCTCCAGAGAAGGATTGTGGGAGA  
 CACTTTTTCTTTCTTTTGCATTAATGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAAGGACG  
 ACAAAGAATTTGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTGTGGGCTTTTTTAC  
 AACAGAAATCAAATCTCCGCTTTGCTGCAAAAGTAACCCAGTTGCACCCTGTGAAGTGTCTGACA  
 AAGGCAGAATGCTTGTGAGATTATAAGCCTAATGGTGTGGAGGTTTTGATGGTGTTTACAATACACT  
 GAGACCTGTTGTTTTGTGTGCTCATTGAAATATTCATGATTTAAGAGCAGTTTTGTAAAAAATTCAT  
 TAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGAGCCTATCAGCAGGGCTCTAGTTTCTAGG  
 AATGCTAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATTATGATACTAGTGAGTACATTAAGTA  
 AAATAAAATGGACCAGAAAAGAAAAGAAACCATAAATATCGTGTCAATTTTCCCCAAGATTAACCA  
 AAAATAATCTGCTTATCTTTTTGGTTGTCCTTTTAACTGTCTCCGTTTTTTTTCTTTTATTTAAAAAT  
 GCACTTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCCTTTGCAAGCCTTACAAGAGA  
 GCACAAGTTGGCCTACATTTTTTATATTTTTTAAGAAGATACTTTGAGATGCATTATGAGAACTTTCA  
 GTTCAAAGCATCAAATGATGCCATATCCAAGGACATGCCAAATGCTGATTCTGTGTCAGGCACTGAAT  
 GTCAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGACGTACAGATACTTTCTCTGAA  
 GAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGACACTTTCTGCTTTACAGAA  
 AAGGAAACTCATTGAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCACATTTCTCCTCA  
 GAAGTAGGGACCGCTTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACAATCTCT  
 TTTCAAACAGGGTGCTCCTCCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAAATATATATAT  
 ATATATATATATTGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTTGTCTACAT  
 GTTATCCACCCAGGCCAGGTGGAAGTAACTGAATTATTTTTTAAATTAAGCAGTTCTACTCAATCA  
 CCAAGATGCTTCTGAAAATTGCATTTTATTACCATTTCAAACATTTTTTTAAAAATAAATACAGTTA  
 ACATAGAGTGGTTTTCTTCATTCATGTGAAAATTATTAGCCAGCACCAGATGCATGAGCTAATTTCT  
 CTTTGAGTCTTCTGCTTCTGTTTGGCTCACAGTAACTCATGTTTTTAAAGCTTCAAGAACATCAAGC  
 TGTGGTGTGTTTAAAAAATGCATTGTATTGATTTGTACTGGTAGTTTTATGAAATTTAATTAACAC  
 AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

**FIGURE 276**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSPTGKEGYQAVLQ  
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL  
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDELVEAIES  
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP  
MKVKNEKLNMAN TLINVI VPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK  
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLN TCR  
LNTQPGKKVFYPVLFSQYNPGIIYGHDAVPPLEQQLVIKKETGFWRDFGFGMT CQYRSDFI  
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTP EQYKMCMQS  
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

**FIGURE 277**

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGA CTGCCATTCATGCTGAACTCTGTCAACC  
AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT  
ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA  
GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT  
ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC  
AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAC  
CTGGAATTTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG  
GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT  
CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT  
AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG  
GGGCATATTAATGATGCCTTCATTGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT  
TGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA  
CCAAGAGCAGATCATATATTTTGTTCACCATTCTTCTTTTGTAAATAAATTTTGAATGTGCT  
TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC  
TCAAATATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG  
TAGTTATTGATTTAAGCATTTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACTTC  
AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT  
TGAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG  
TGAGAAGTAATTATTGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATT  
TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC  
AATTCTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG  
TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA



**FIGURE 279**

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG  
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**  
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG  
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC  
 TCGGTTAAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA  
 ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC  
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA  
 TGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA  
 AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA  
 CGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT  
 AATAGTAATTGTAGTGGTCCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC  
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT  
 GTTTATTTAGAAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA  
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT  
 TTTCCAACCAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC  
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA  
 GTGTAAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAA  
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC  
 AATTTGTCTGTTACATTTTCCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA  
 ATGTGTTTACTCTCTTTCCTTCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTG  
 TTTCTGATTAACAGTAAATCCTAAATTCAAACGTGTTAAATGACATTTTTATTTTTATGTCTC  
 TCCTTAACTATGAGACACATCTTGTTTTACTGAATTTCTTCAATATTCCAGGTGATAGATT  
 TTTGTCG

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**FIGURE 280**

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT  
WNFRPLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ  
VKNPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLQHYRKKRWAER  
AHKVVEIKSKEERLNQEKKVSVYLEDTD

050743 44604



GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT  
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG  
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT  
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG  
TAAAGACATTCCAGTTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCTT  
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAAC TATTCATGCTTCCTGTGATTC  
ATCCAACTACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA  
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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**FIGURE 282**

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT  
 TAASTTARKDIPVLPKWVDLPNGRVCP

| Parameter          | Unit | Value | Unit | Value |
|--------------------|------|-------|------|-------|
| Mean               | mm   | 1.5   | mm   | 1.5   |
| Standard deviation | mm   | 0.5   | mm   | 0.5   |
| Minimum            | mm   | 0.5   | mm   | 0.5   |
| Maximum            | mm   | 2.5   | mm   | 2.5   |
| Range              | mm   | 2.0   | mm   | 2.0   |
| Median             | mm   | 1.5   | mm   | 1.5   |
| Mode               | mm   | 1.5   | mm   | 1.5   |
| Skewness           |      | 0.0   |      | 0.0   |
| Kurtosis           |      | 0.0   |      | 0.0   |
| Mean               | mm   | 1.5   | mm   | 1.5   |
| Standard deviation | mm   | 0.5   | mm   | 0.5   |
| Minimum            | mm   | 0.5   | mm   | 0.5   |
| Maximum            | mm   | 2.5   | mm   | 2.5   |
| Range              | mm   | 2.0   | mm   | 2.0   |
| Median             | mm   | 1.5   | mm   | 1.5   |
| Mode               | mm   | 1.5   | mm   | 1.5   |
| Skewness           |      | 0.0   |      | 0.0   |
| Kurtosis           |      | 0.0   |      | 0.0   |
| Mean               | mm   | 1.5   | mm   | 1.5   |
| Standard deviation | mm   | 0.5   | mm   | 0.5   |
| Minimum            | mm   | 0.5   | mm   | 0.5   |
| Maximum            | mm   | 2.5   | mm   | 2.5   |
| Range              | mm   | 2.0   | mm   | 2.0   |
| Median             | mm   | 1.5   | mm   | 1.5   |
| Mode               | mm   | 1.5   | mm   | 1.5   |
| Skewness           |      | 0.0   |      | 0.0   |
| Kurtosis           |      | 0.0   |      | 0.0   |
| Mean               | mm   | 1.5   | mm   | 1.5   |
| Standard deviation | mm   | 0.5   | mm   | 0.5   |
| Minimum            | mm   | 0.5   | mm   | 0.5   |
| Maximum            | mm   | 2.5   | mm   | 2.5   |
| Range              | mm   | 2.0   | mm   | 2.0   |
| Median             | mm   | 1.5   | mm   | 1.5   |
| Mode               | mm   | 1.5   | mm   | 1.5   |
| Skewness           |      | 0.0   |      | 0.0   |
| Kurtosis           |      | 0.0   |      | 0.0   |
| Mean               | mm   | 1.5   | mm   | 1.5   |
| Standard deviation | mm   | 0.5   | mm   | 0.5   |
| Minimum            | mm   | 0.5   | mm   | 0.5   |
| Maximum            | mm   | 2.5   | mm   | 2.5   |
| Range              | mm   | 2.0   | mm   | 2.0   |
| Median             | mm   | 1.5   | mm   | 1.5   |
| Mode               | mm   | 1.5   | mm   | 1.5   |
| Skewness           |      | 0.0   |      | 0.0   |
| Kurtosis           |      | 0.0   |      | 0.0   |
| Mean               | mm   | 1.5   | mm   | 1.5   |
| Standard deviation | mm   | 0.5   | mm   | 0.5   |
| Minimum            | mm   | 0.5   | mm   | 0.5   |
| Maximum            | mm   | 2.5   | mm   | 2.5   |
| Range              | mm   | 2.0   | mm   | 2.0   |
| Median             | mm   | 1.5   | mm   | 1.5   |
| Mode               | mm   | 1.5   | mm   | 1.5   |
| Skewness           |      | 0.0   |      | 0.0   |
| Kurtosis           |      | 0.0   |      | 0.0   |
| Mean               | mm   | 1.5   | mm   | 1.5   |
| Standard deviation | mm   | 0.5   | mm   | 0.5   |
| Minimum            | mm   | 0.5   | mm   | 0.5   |
| Maximum            | mm   | 2.5   | mm   | 2.5   |
| Range              | mm   | 2.0   | mm   | 2.0   |
| Median             | mm   | 1.5   | mm   | 1.5   |
| Mode               | mm   | 1.5   | mm   | 1.5   |
| Skewness           |      | 0.0   |      | 0.0   |
| Kurtosis           |      | 0.0   |      | 0.0   |
| Mean               | mm   | 1.5   | mm   | 1.5   |
| Standard deviation | mm   | 0.5   | mm   | 0.5   |
| Minimum            | mm   | 0.5   | mm   | 0.5   |
| Maximum            | mm   | 2.5   | mm   | 2.5   |
| Range              | mm   | 2.0   | mm   | 2.0   |
| Median             | mm   | 1.5   | mm   | 1.5   |
| Mode               | mm   | 1.5   | mm   | 1.5   |
| Skewness           |      | 0.0   |      | 0.0   |
| Kurtosis           |      | 0.0   |      | 0.0   |
| Mean               | mm   | 1.5   | mm   | 1.5   |
| Standard deviation | mm   | 0.5   | mm   | 0.5   |
| Minimum            | mm   | 0.5   | mm   | 0.5   |
| Maximum            | mm   | 2.5   | mm   | 2.5   |
| Range              | mm   | 2.0   | mm   | 2.0   |
| Median             | mm   | 1.5   | mm   | 1.5   |
| Mode               | mm   | 1.5   | mm   | 1.5   |
| Skewness           |      | 0.0   |      | 0.0   |
| Kurtosis           |      | 0.0   |      | 0.0   |
| Mean               | mm   | 1.5   | mm   | 1.5   |
| Standard deviation | mm   | 0.5   | mm   | 0.5   |
| Minimum            | mm   | 0.5   | mm   | 0.5   |
| Maximum            | mm   | 2.5   | mm   | 2.5   |
| Range              | mm   | 2.0   | mm   | 2.0   |
| Median             | mm   | 1.5   | mm   | 1.5   |
| Mode               | mm   | 1.5   | mm   | 1.5   |
| Skewness           |      | 0.0   |      |       |

**FIGURE 283**

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC  
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**  
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA  
GTGTCCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC  
ACTTGGAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG  
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG  
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT  
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAAA**ACCACAGGCTGG  
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA  
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAACTGAGAAAT  
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT  
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA  
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG  
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT  
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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**FIGURE 284**

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG  
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPFVGVARGGALCQ

FIGURE 284

**FIGURE 285**

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA  
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG  
GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA  
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTGAGC  
CGGGGCCGGGATGCAGCCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA  
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCCAGGCACAGA  
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT  
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC  
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC  
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCCTGAATCTGCCTGGATGGAAGTGA  
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG  
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC  
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA  
CCCTTTCATGCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 286**

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLT  
K  
ARNSLGLYGRITIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK  
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ  
IQERLHTAALPA

Figure 1 consists of 12 subplots (a-l) showing the time course of various physiological and behavioral parameters during the first 24 hours of a 28-day study. The parameters are: (a) Rectal temperature (°C), (b) Core temperature (°C), (c) Heart rate (b/min), (d) Minute ventilation (l/min), (e) Oxygen consumption (ml/min), (f) Energy expenditure (kcal/min), (g) Energy expenditure (kcal/kg), (h) Energy expenditure (kcal/kg), (i) Energy expenditure (kcal/kg), (j) Energy expenditure (kcal/kg), (k) Energy expenditure (kcal/kg), and (l) Energy expenditure (kcal/kg). Each graph compares two groups: Control (solid line) and Experimental (dashed line). The x-axis represents time in hours from 0 to 24. The y-axis represents the parameter value. Error bars represent standard error of the mean (SEM).

Figure 1 consists of 12 subplots (a-l) showing the time course of various physiological and behavioral parameters during the first 24 hours of a 28-day study. The parameters are: (a) Rectal temperature (°C), (b) Core temperature (°C), (c) Heart rate (b/min), (d) Minute ventilation (l/min), (e) Oxygen consumption (ml/min), (f) Energy expenditure (kcal/min), (g) Energy expenditure (kcal/kg), (h) Energy expenditure (kcal/kg), (i) Energy expenditure (kcal/kg), (j) Energy expenditure (kcal/kg), (k) Energy expenditure (kcal/kg), and (l) Energy expenditure (kcal/kg). Each graph compares two groups: Control (solid line) and Experimental (dashed line). The x-axis represents time in hours (0 to 24). The y-axis represents the parameter value. Error bars represent standard error of the mean (SEM).

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**FIGURE 288**

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHKKRRVRDKDGDGLKTQIEKLWT  
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ  
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK  
WSDEACRSSKRYICEFTIPK

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**FIGURE 289**

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC  
CCCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA  
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTG  
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCT  
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT  
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG  
GCCCTGACAGTGTTTGGC**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC  
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCGGCCCCCT  
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

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**FIGURE 290**

MKLAALLGLCVALSCSSAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLLLS  
SLGIPVNHLEGSQKCVAELGPQAVGAVKALKALLGALTVFG

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**FIGURE 291**

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT  
 CCTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTG  
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCCTCAGTCGCCAGAGACCCCAGCCCC  
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGG  
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT  
 GCCAAGGAGACTTCAAACCTTCGGATTACAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG  
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA  
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG  
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAC  
 GGGCCTCTCACAGGGGAGTTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT  
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCGTGCCTATGAATTTTCGCAATGCCTCA  
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTCCCAAAC  
 GTTTGATGAGATTAATCCTGAAACCAAATTAATTCTTGTGGATTACATCTTGTTCAAAGGGA  
 AATGGTTGACCCATTTGACCCTGTCTTCACCGAAGTCGACACTTTCCACCTGGACAAGTAC  
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA  
 TTTTCGTTGTCTGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA  
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA  
 TGGCTCAGAAACATGAAAACCAGAAACATGGAAGTTTTCTTCCGAAGTTCAGCTAGATCA  
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCCTTG  
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA  
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTCAGAAATTAC  
 TGCTTATTCATGCCTCCTGTCATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG  
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTAT**TA**ATTAGG  
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA  
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCCTTTTGTCTTAACTAGTTTAGGGTGTCTC  
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGGATACATTCAAAGACCCCCAGCAGATGC  
 CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT  
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA  
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA  
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA  
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCCTACTCAGAATGGCATGC  
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTTTCATTTAATGTTTTTGGACCATGGT  
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA  
 GCATTAAATTGATACATATTTTTTTAAAAA

MKVVPSLLLSVLLAQVWLVPG LAPSPQSPETPAPQNQTSRVVQAPREEEEDQEASEEKAGE  
 EEKAWLMASRQQ LAKETS NFGFSLLRKISMRHDGNMVFSPFGMSLAMTGLMLGATGPTETQI  
 KRGLHLQAL KPTKPGLLP SLFKGLRETL SRNLELGLSQGSFAFIHKDFDVKETFFNL SKRYF  
 DTECVPMNFRNASQAKRLMNHYINKETRGI PKLFDEINPETKLILVDYILFKGKWLTPFDP  
 VFTEVDTFHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHL  
 ALEDYLTDDL VETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRI FSPFADLSELSA  
 TGRNLQVSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIEETSGMLLF  
 LGRVVNPTLL

**FIGURE 293**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGAC**ATGAG**  
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG  
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG  
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCCC  
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA  
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCCTGAGTCCC  
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCCTGAGGAGGACCAGGGCGAGGAGAGGCC  
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA  
TCTACCACCCCCAG**TAG**GGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGG  
CTGTTGGGACTGGGACCCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCCAGCAGGCAA  
AAAAAAAAAAAAAAAAA

**FIGURE 294**

MRLLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL  
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE  
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

FIGURE 294

**FIGURE 295**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG  
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC  
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA  
TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC  
TAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT  
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG  
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC  
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG  
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG  
CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC  
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT  
ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGC  
GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATT  
TGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG  
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT  
CCCCAGCAGTGTGGAGATTTTTCTGGTTTTGATTGGAGTGGATATGGAACATCATGTTGGTTA  
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG  
GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCA  
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

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**FIGURE 296**

MNQLSFLLEFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN  
GVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG  
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGL  
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSYPYGQREFTAGFVQFRVFNNERAAN  
ALCAGMRVTGCNTEHHCIGGGGYFPEASPOQCDFSGFDWSGYGTHVGYSRSSREITEAAVLL  
FYR

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**FIGURE 297**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC  
CACGAGGCTGCCGCATCCTGCCCTCGGAACA**ATG**GGACTCGGCGCGCGAGGTGCTTGGGCCG  
CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC  
ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC  
AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC  
CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG  
GCATCTAATAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC  
TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG  
TAACCCACAATAGTTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT  
TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC  
GCTGGGAGTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC  
GGTATCGAACCATAGATGAACATGATGCCATCATT**TAAG**GAAATCCATGGACCAAGGATGGA  
ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCT  
CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA  
AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT  
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTTGGCT  
GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA  
TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT  
AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA  
CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG  
TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

**FIGURE 298**

MGLGARGAWAALLLGTQLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVP  
SDH  
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQ  
N  
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG  
CKMYYSRRGIRYRTIDEHDAII

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CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG  
TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCG**ATG**GCGACCCTGTGGGGAGGC  
CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTTCGTGCCTGGCGCTTTCGGTGCTGCTGCTGGC  
GCAGCTGTCAGACGCCGCCAAGAATTTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCT  
ATAAAGAAAATTTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT  
CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA  
ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA  
TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATCTGAAGAGG  
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT  
TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG  
AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG  
CATGTTGTCTCTCAGC**TAA**ATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA  
CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTTCATTTTAATACCTTGTTGATTTACCAACT  
GTTGCTGGAAGATTCAAAACCTGGAAGCAAAAACCTTGCTTGATTTTTTTTTTCTTGTTAACGTA  
ATAATAGAGACATTTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCCTATTTG  
TGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA  
AGCACTCTCTTTTTTACCACATAGTTTTTAACCTTGACTTTCAAGATAATTTTTCAGGGTTTTTG  
TTGTTGTTGTTTTTTTGTGTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT  
AACAACTTTTTTCAAGTCACTTTACTAAACAAACTTTTTGTAAATAGACCTTACCTTCTATTT  
TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG  
ACTTTTGCACCTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGAT  
CTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG  
CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG  
GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT  
TGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTG  
TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACT  
AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT  
TCTTCCTATGTCCTCTTTGGGAATGTAACAATAAAAAATAATTTTTTGAACATCAA

**FIGURE 300**

MATLWGGLRLGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS  
GHINKNISQKDCDLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKV  
TIIYLSILGLLLLYMVYLTLEVPIPKRRLFGHAQLIQSDDDIGDHQPF  
ANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQRKSVFDRHVLS

Figure 1 displays Northern blot analysis of 18S rRNA and GAPDH mRNA levels in various tissues. The figure is organized into 12 panels, with the first six panels showing 18S rRNA levels and the next six panels showing GAPDH mRNA levels. Each panel contains four lanes, labeled 1, 2, 3, and 4, representing different tissues: (1) testis, (2) epididymus, (3) vas deferens, and (4) spermatozoa. The blots show varying levels of expression across the tissues and conditions.

[illegible]

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**FIGURE 302**

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGRFPPMMHHHQAPSDGQT  
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFGLYILYILFKVSRIILI  
ILHQ

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**FIGURE 303**

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT  
GGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTAC  
TGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTG  
GGTGATTAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT  
AGACTGGACTCTGTACCAAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA  
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGC  
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA  
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG  
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG  
AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA  
GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGG  
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCATCATG  
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT  
GGTGTTCAAGAAAACCATTTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCC  
CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC  
TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA  
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG  
AAAAACCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA  
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA  
CCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG  
GAATGCCAAAAACACAGCAAGCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG  
TGGAGACTCTCTCCTGTGTGTGTCTCTGGGCCACTCTACCAGTGATTTAGACTCCCGCTCTC  
CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG  
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC  
CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTT  
GGATCAGACCCTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA  
AAAACCAACCCAAATCAA

**FIGURE 304**

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCI FKIDWTLSPG  
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGT YICEIRLKGES  
QVFKKAVVLHVLPEEPKELMVHVGGGLIQMGCVFQSTEVKHVT KVEWIFSGRRAKEEIVFRYY  
HKL RMSVEYSQSWG HFQNRVNLVGDIFRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV  
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLLPVLILIVKKT CGNKSSVNSTV  
LVKNTKKTNPEIKEKPC HFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR  
SDRNN SLEKKS GGGMPKTQQAF

T05T" E092660



**FIGURE 305**

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG  
GTTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG  
AAACTACATTTTGGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATGCA**  
GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG  
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG  
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGA  
TGAGAATGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG  
TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC  
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG  
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG  
AGTACATCAAAGCCAGGACTCATTTAATTCGTGGGTCGGATTATCTCGCCAGAAGTCGAAT  
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA  
TGGAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG  
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT  
**TAA**TGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT  
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

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**FIGURE 306**

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRNYL  
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE  
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEEFL  
EDGKGNMNCAYFHNGKMHPTFCENKHLYLMCERKAGMTKVDQLP

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## **FIGURE 307**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG  
CCCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC  
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAA  
GCCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG  
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG  
CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG  
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC  
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG  
AAGAAGACCAGAGCCTCAGCTTAAGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC  
ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACT  
CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT  
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA  
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG  
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA  
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT  
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC  
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC  
**GTAG**CCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT  
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG  
CAGAGTTCATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

0997661-11501

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## **FIGURE 308**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCDKNKLNVFSRVKLFSGSKRRRRRP  
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA  
MNSEGILYTSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK  
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMSHNEST

### **N-glycosylation site.**

amino acids 242-246

### **Glycosaminoglycan attachment site.**

amino acids 165-169, 218-222

### **Tyrosine kinase phosphorylation site.**

amino acids 93-100

### **N-myristoylation site.**

amino acids 87-93, 231-237

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 231-239

### **HBGF/FGF family proteins**

amino acids 78-94, 102-153

**FIGURE 309**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG  
ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG  
CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAAGTGGGGGATCCCCCT  
CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTGGGTTCCCTTCTGACATTGGCAGTG  
CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC  
AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA  
ACCACGTCTTGGAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG  
GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCCAAACTCGAGGGTGGGATCCACTGAGG  
AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCT  
GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG  
CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAG  
CGCGCTCCGGGCGCCTGCCGTTTGGGGGTGTCTCCTCCCGGGGCGCT**ATG**GCGGCGCTGGC  
CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCG  
CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG  
CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCGCGCGGCCGGACCGCGGCCCGGAGCCTCA  
GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCCG  
ACGGAAGCATCCAGGGCACCCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT  
GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC  
TGAGGGACTGCTCTACAGTTCGCCGCATTTCACAGCTGAGTGTGCTTTAAGGAGTGTGTCT  
TTGAGAATTACTACGTCCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC  
TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAA  
GGCAGCTGCCCACCTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC  
ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCC**TGA**AATGTAGTCCCTGGACTG  
GAGGTTCCCTGCACTCCCAGTGAGCCAGCCACCACCACAACCTGT

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## **FIGURE 310**

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR  
GPEPQLKGIVTKLFCRQGFYQLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY  
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR  
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

### **Tyrosine kinase phosphorylation site:**

amino acids 199-207

### **N-myristoylation sites:**

amino acids 54-60, 89-95, 131-137

### **HBGF/FGF family signature:**

amino acids 131-155

**FIGURE 311**

**ATG**GCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG  
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG  
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG  
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT  
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT  
TCAACCTCATAACAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT  
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT  
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG  
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA  
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG  
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA  
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

**FIGURE 312**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR  
RQDPQLKGIVTRLYCRQGYLQMHDPGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY  
IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR  
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSITT

**N-glycosylation site.**

amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site.**

amino acids 199-207

**N-myristoylation site.**

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins.**

amino acids 104-155, 171-198



**FIGURE 313**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAT  
 GAAGGATGCAGGACGCAGCTTTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA  
 ACGAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG  
 AAATAAACAGACTTAGACCCGCGGGGGTTGGTGTGTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCC  
 CTCCCCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCAGGATTACAAAAGAAAAAGTATGTTTCATTT  
 TTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA  
 AGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAAGAGGAGAGGAAATTAATAATACATCTGC  
 AAAGAAATTTAGAGAGAAGAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCA  
 CAGTTGGATTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT  
 TTTTTAAATTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACCTGGATTTCATCT  
 GGATGTTGCTGTGATCAGTCTGAAATACAATGTTTGAATTCAGAAGGACCAACACCAGATAAATTATGAATC  
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAACAGGGCCCTATTTGACCCCT  
 GCTTGTGGTGTCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGC GGCTCAGACCTGCCCTTCTGTGT  
 GCTCCTGCAGCAACCAGTTCAGCAAGGTGATTTGTGTTTCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC  
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAG  
 GCACTTGGAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGA  
 ACCTCAACACTCTGGAACCTTTGACAACTGCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAA  
 CTGAAGGAGCTCTGGTTGCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTTAACAGAATTCCTTCTTT  
 GCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAAT  
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAG  
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAAAT  
 GTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCA  
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT  
 TTACATCACAAACCTTGAACTGTAAGTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC  
 GAACACAGCTTGTGTGCCCCGTGTAACACTCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA  
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCT  
 GAGCTGAAATGTGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA  
 TGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTAAATTTACAAATGTAAGTGTGCAAGATA  
 CAGGCATGTACACATGTATGGTGAGTAATTCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCA  
 GCAACCACTACTCCTTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG  
 GACCACAGATAACAATGTGGGTCCCCTCCAGTGGTGGTGGAGACCACCAATGTGACCACCTCTCTCACAC  
 CACAGAGACAAGGTGACAGAGAAAACCTTACCATCCCAGTGAATGATATAAACAGTGGGATCCCAGGAATT  
 GATGAGGTCATGAAGACTACCAAAATCATCATTTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT  
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTA  
 TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAG  
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTCATACA  
 CAGTTCAGTGATGAACCGTTATTGATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATCTAAACAA  
 TTTACAGAGTTACAAAAACAAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAA  
 ATCTACTGTTTTCAAAAAAGTGTCTTTACAAAAAACAAGAAAGAAATTTATTTATTAATAATCTATTG  
 TGATCTAAAGCAGACAAAAA

**FIGURE 314**

MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
 VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
 NLNTELEFDNRLTTIPNGAFVYLSKLLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
 YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLELDL SGNHLSAIRPGSFQGLMHLQKL  
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDIL  
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
 LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLS DGTNLNFTNVTVQDTGMYTCMVNSVGN  
 TTASATLNVTAATTT PFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTS LTPQ  
 STRSTKFTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
 HHAPTRTVEIINV DDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
 VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,  
 434-438, 442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
 391-397, 422-428, 433-439, 531-537

**FIGURE 315**

GCGCCGGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT  
 GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTGCGA  
 GCGCCCGGGCGCCCGCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC  
 GGG**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCCCTACTATGTTGGAACCTTGGGGACTCA  
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC  
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
 AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGC  
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT  
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATT  
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT  
 GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA  
 CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACGTGTACAGT  
 ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
 ATTTTCTCCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT  
 CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAAT  
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC  
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG  
 CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA  
 ACGGTCT**TGA**ATTACAATGGACTTGACTCCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC  
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
 GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTTCTTATAACAATACCAACAAGCAAA  
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
 AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
 AGGTGAATATACCTAAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT  
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACCTTATTGGATT  
 ATTAGTTATTACAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
 TGAGCTAACCCTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
 TTCATTTGTCAATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC  
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT  
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCTCAAAT  
 CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT  
 TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
 CCAACATACCATTATAGTCTCTTCTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG  
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
 TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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## **FIGURE 316**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251

Figure 316





**FIGURE 319**

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA  
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC  
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGC  
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG  
 AGAG**ATGA**AATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC  
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTG  
 CTTCTCTGGAGCCAGGTATCAGGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT  
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG  
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT  
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAACGTGTTTTCAAAAA  
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC  
 TTGTTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC  
 AGTGCACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC  
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGC  
 TC**TGA**ATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTTCA  
 AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT  
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG  
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTT  
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG  
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG  
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT  
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACTGAACTTCAGAGCATGAAAATCACACT  
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAAGGTGCATCTGTTTGAAAAG  
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT  
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT  
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC  
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCTTGCTAATAAAAGACAACATAA  
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 320**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFCCPPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGGQEFHFGPCQVK  
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH  
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL  
TKALGEVDILLTWMQKFYKL

### **Signal sequence:**

amino acids 1-42

### **N-glycosylation sites.**

amino acids 85-89, 99-103, 126-130

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**FIGURE 321**

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC  
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC  
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG  
ACACCTTCCCAAATGTCACCTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA  
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA  
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA  
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC  
AATGCCACCAGAGTCATCCATGACAACCTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT  
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC  
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT  
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT  
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

**FIGURE 322**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282  
><subunit 1 of 1, 177 aa, 1 stop  
><MW: 20452, pI: 8.00, NX(S/T): 2  
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST  
LETIQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ  
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

**Signal sequence:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 56-60, 135-139

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation site.**

amino acids 24-30

**Actinin-type actin-binding domain signature 1.**

amino acids 159-169

TCSTT " 634660

**FIGURE 323**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG  
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT  
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC  
GGTTCATATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCCGCCT  
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA  
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC  
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC  
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA  
TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTTGGATCACACTATTTTCGAC  
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC  
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC  
CACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACC  
CCCATAACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT  
GCTGAAGCCCCGGGCCCCGGATGACCCCGGCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG  
CCGAGGACAACAGCCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCGAGTGAAC  
ACGCACGCTGGGGGAACGGGCCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCTG  
CTGG

**FIGURE 324**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWGGLIHLYTATARNSYHLQIHKNGHVD  
 GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY  
 DVIHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSE  
 RDPLNLVKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTTHAGGTGPEGCRPFA  
 KFI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 175-179

**N-myristoylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124

**FIGURE 325**

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**  
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG  
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG  
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG  
 ACCTCTTCTAGGGCCTCAACCCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA  
 GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTACAAAAACATCTCCCAACTTCATGGTGC  
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC  
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA  
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA  
 CAGAAGCTAAGGGCCTGTCCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC  
 ACCCGCTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC  
 GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT  
 GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTACAAACATCGAG  
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGA  
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC  
 CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTCACAGCCTCTGCCGAGACCCTGTCC  
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA  
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA  
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC  
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTC  
 CTTTGCTGGGAGCTCTGCTTCTCCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC  
 CTTTACAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCT  
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA  
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC  
 GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAAATGGAGGTTTCTCCTCCTGCGGCTGAGTG  
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC  
 CGGGAACCTCCACGCCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA  
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCCTAGCCTG  
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG  
 AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC  
 CGGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCAGAGGTGTCTTGGACTCACCTTGG  
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA  
 TTTAAATTCACTCAGTGTGGCCCAAAAAA

**FIGURE 326**

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL  
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSNFMVLIATSVETSAASGSPEGAGM  
 TTVQTTITGSDPEEAIFDTLCTDDSSSEAKTLTMDILTTLAHTSTEAKGLSSESSASSD  
 GPHPVITPSRASESSASSD  
 GPHPVITPSRASESSASSD  
 GPHPVITPSWSPGSDVTLLAEALVTVTNI  
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASA  
 ETLSTAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLSGALVTVSRNPLEETSALS  
 VETPSYVKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPPSEAALKNFTPSETPTMDI  
 ATKGPFPPTSRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT

**N-glycosylation sites:**

amino acids 252-256, 445-449, 451-455

**cAMP-and cGMP-dependent protein kinase phosphorylation site.**

amino acids 84-90

**Casein kinase II phosphorylation sites.**

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,  
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,  
 404-408, 414-418, 431-435

**N-myristoylation sites.**

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-  
 320, 349-355, 386-392, 397-403, 449-455

**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

**FIGURE 327**

GCGGAGCATCCGCTGCGGTCTCTCGCCGAGACCCCCGCGCGGATTTCGCCGGTCTTCCCCGCGG  
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA  
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT  
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAAATGTTCTTCGGGGGAGAAGGGAG  
 CTTGACTTACACTTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC  
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC  
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA  
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA  
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCC  
 TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT  
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA  
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTACAATTTTCTCTGATCAAGAAA  
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
 CATAACCTCGGCTACTCCAAAGCCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC  
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
 AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG  
 GCTACAACAGCAGTTCTGACTACCACCTTTAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
 AACCATAACGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCTA  
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCCTGGGAAGGT  
 AGGGAGGCCAGTCCAGGCAGTTCCTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC  
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTCTGTTCTGTTGATAGGCC  
 TCGTCTCTGTTGGGTAGAATCCTTTCCGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT  
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT  
 TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG  
 TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCCTTTTTTTTTTTTGGAGACAGAGTCTT  
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC  
 CTGGGTTCAAGCGATTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
 CCACACCTGGGTGATTTTTGTATTTTTTAGTAGAGACGGGGTTTACCATGTTGGTCAAGCTG  
 GTCTCAAACCTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG  
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTTGGTTTTTGGAGAAGGAATGAAGTG  
 GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAAATATTAGCTAAAAACAAAGCTCT  
 ATGTAAAGTAATAAAGTATAAATTGCCATATAAATTTCAAAATTCAACTGGCTTTTATGCAA  
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGTTCCAGATAAAATCAAC  
 TGTTTATATCAATTTCTAATGGATTTGCTTTTCTTTTATATGGATTCTTTTAAACTTATT  
 CCAGATGTAGTTCTTCCAATTAAATATTTGAATAAATCTTTTGTACTCAA

**FIGURE 328**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFPGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLKGI RGN EPVYTSTQED  
CINSCCSTKNISGDKACNLMI FDTRKTARQPN CYLFFCPNEEACPLKPAKGLMSYRIITDFP  
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF  
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPH TTSATPKPATLL  
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTTFQAP  
TDSKGSLETIPFTEISNLTNLNTGNVYNPTALSMSNVESSTMNK TASWEGREASPGSSSQGSV  
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRY S RLDYLINGIYVDI

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321



**FIGURE 329**

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT  
 CCCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT  
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA  
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG  
 TCTTTACTGATCTCTCTGTTCTCTTTCCAGGACCCTGCTGTCCTCCCTCCCCTTCTCCCAC  
 CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCCAAGGCAAAAGCTCAGCAAACCCAGC<sup>CCC</sup>  
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCATGCAGC  
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTGCTGAGCCTTCTGTGAGC  
 CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC  
 CCTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA  
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT  
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG  
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGATGTTCCA  
 GCCTGACCTAGAAGCGTTTGTCTCAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA  
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTTGGGC  
 CTCATGCCCAGTGTGCGACCCTGCCTTCCCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC  
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGATGAAGAGGAGCATGCT  
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT  
 GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
 GACTCTGAATTCTAACAATGCCAGTGACTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTG  
 ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC  
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGACTCCCCTGAGGCCTGCTAAG  
 TCCAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG  
 TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAATGATGAAGA  
 AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA  
 GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA  
 GCACAACCTACTATTTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT  
 GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCCTCCTGGGTTCAAGTGATT  
 CTTCTGCCTCAGCCTCCCAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT  
 TTTGTACTTTTAGTAGAGATGGGGTTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCTGAC  
 CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG  
 TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCAAGTATGCAAAACTTGGAAAG  
 ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT  
 TATTTCTGTTTTGTTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTTCTT  
 TTTACAGAGCAATTATCTTGTATATACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
 ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTATAAATAAAATGTTTCATCA  
 GCTGCATAAAAAAAAAAAAAA

**FIGURE 330**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPTEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSIRDSTRQELSLIVTLWNLTLDAGEYWCGVEKRGPDSELLISLFV  
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEPPLPG  
TSQYGHERTSQYTGTSPHPATSPPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETORNEKFWLSRLTAEKEAPSQAPEGD  
VISMPPLHTSEEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128